```
SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=C57BL/60; TISSUE=Adipose tissue;

MEDININE=2534683; PubMed=12466851; DOI=10.1038/nature01266;

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Fagark, Y., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Radarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Raladarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Randian I.M., Kanapin A., Matsud H., Ratadov S., Beisel K.W., Baldarelli B., Dragami T.A., Fletcher C.F., Forrest A., Frazer K.S., R.A Dalla E., Dragami T.A., Fletcher C.F., Forrest A., Gough J., R. Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J., R. Aranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., R. Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., R. Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Ramachandra T., Numata K., Pontius J.U., Qi D., Ramachandran S., Pesole G., R. Arasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Schneider C., Semple C.A., Sectou M., Shimada K., Shimada K., Ashanda R., Takenaka Y., Taylor M.S., Taesdale R.D., Tomita M., Vang L., Wallang L.G., Wang I., Yang L., Yang L., Yang L., Xang L., Yang L., Xang L., Xan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIT2_MOUSE STANDARD;
QFRB93; QTTR15; QB12K5; Q99MB1;
QFRB93; QTTR15; QB12X1; Q22X5; Q99MB1;
01-0CT-2004 (Rel. 45, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
01-0CT-2004 (Rel. 45, Last sequence update)
01-0CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                 Cytoplasmic (Potential).
Signal-anchor for type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 128.5; DB 1; Length 558;
                                                                                                                                                                               stack; Lectin; Manganese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 CGGSLEIVPCSRVGHVFRKRHPYNPPEGNALTYIRNTKRTAEVWM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLA--RNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Colon adenocarcinoma,
Miyahara N., Kanoh A., Irimura T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2FE9B0CAD13FC8AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Catalytic subdomain A. Catalytic subdomain B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricin. B-type lectin. By similarity. By similarity. By similarity. By similarity.
                                                                                                                                                                                                                                                                                                                  protein (Potential)
Lumenal (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.9e-09;
6; Mismatches 11
InterPro; IPR000772; Ricin_B lectin.
Pfam; PF00535; Glycos transf_2; 1.
Pfam; PF00652; Ricin_B lectin; 2.
SWART; SMO0458; RICIN_F 1.
Calcium; Glycosyltransferase; Golgi stack;
Signal-anchor; Transferase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63019 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 55.6
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             558 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                    122
286
428
441
530
                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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GLT2 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hippocampus.
DOMAIN: There are two conserved domains in the glycosyltransferase region: the N-terminal domain (domain A, also called GTI motif), which is probably involved in manganese coordination and substrate binding and the C-terminal domain (domain B, also called Gal/GalNac-T motif), which is probably involved in catalytic reaction and UDP-Gal binding (By similarity).

DOMAIN: The ricin B-type lectin domain binds to GalNAc and contributes to the glycopeptide specificity (By similarity).

SIMILARITY: Belongs to the glycosyltransferase family 2. GalNAc-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissur spiritury: In the CNS, it is predominantly expressed in several distinct hypothalamic, thalamic and amygdaloid nuclei. The most abundant level of expression is in the paraventricular, ventromedial and arcuate nuclei of the hypothalamus, the anterodorsal and parafascicular nuclei of the thalamus and the central, basomedial and medial nuclei of the amygdala. Also expressed in cerebral cortex, lateral septum, habenula and
                                                                                       01-0cT-2004 (Rel. 45, Created)
01-0cT-2004 (Rel. 45, Last sequence update)
01-0cT-2004 (Rel. 45, Last sequence update)
Putative polypeptide N-acetylgalactosaminyltransferase-like protein 1 (EC 2.4.1.41) (Protein-UDP acetylgalactosaminyltransferase-like protein 1) (UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-like like protein 1) (Polypeptide GalNAc transferase-like protein 1) (Polypeptide GalNAc transferase-like protein 1) (Polypeptide GalNAc transferase-like protein 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelson P.A., Sutcliffe J.G., Thomas B.A.,
"A new UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase mRNA exhibits predominant expression in the hypothalamus, thalamus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 ricin B-type lectin domain.
-!- CAUTION: Was originally (Ref.2) termed Galnt10/pp-GaNTase 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
Hashimoto K.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                    558 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AB045325; BAA97985.1; -.
MGD, MGI:1917754; Galntll.
InterPro; IPR001113; Glyco_trans_2.
InterPro; IPR008997; Richins_like.
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                         Name=Galntl1;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15018805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                         GTL1 MOUSE
Q9JJ61;
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5,

Gaps

ю М

11; Indels

SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

STRAIN-C57BL/6, and Czech II; TISSUE=Brain, and Breast tumor;

XX MIDIINE=2238825; PubMed=12477932; DOI=10.1073/pnes.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Gollins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B.E., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moczer T., Max S.I., Wang J., Hisheh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Roaleston M., Jodin T.B., Toshiyuki S., Carninci P., Prange C.,

Roanstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Morley X.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley X.C., Hale S., Garcia A.M., Gaibbs R.A.,

Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

Whiting M., Madan A., Young A.C., Shevichenko Y., Bouletaffard G.G.,

Hakesley R.W., Touchman J.W., Maran M.M.,

Schrigtez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Manner A., Schehn J.E., Once B.J.M., Marra M.A.,

"Manner A., Schehn J.E., Once B.J.M., Marra M.A.,

"Manner A., Schehn J.E., Once E. J.M., Marra M.A.,

"Manner A., Schehn J.E., Once E. M., Marra M.A.,

"Manner A., Schehn J.E., Once B.J.M., Marra M.A.,

"Manner A., Schehn J.E., Once B.J.M., Marra M.A.,

"Manner A., Manner A., Schehn J.E., Once E. J.M., Marra M.A.,

"Manner A., Schehn J.E., Once B.J.M., Marra M.A.,

"Manner A., Schehn J.E., Once B.J.M., Marra M.A.,

"Manner A., Schehn J.E., Once B.J.M., Marra M.A.,

"Manner A., Manner A., Schehn J.E., Once B.J.M., Marra M.A.,

"Manner A., Manner A., Manner B., Ma Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Komo H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashirume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sakai K., Shihata K., acetylgalactosaminyltranseerisciorms in murine tissues determined by real-time PCR: a new view of a large family.";

Glycobiology 13:549-557(2003)

-1- FUNCTION: Catalyzes the initial reaction in O-linked oligosaccharide biosynthesis, the transfer of an N-acetyl-D-galactosamine residue to a serine or threonine residue on the protein receptor. Has a broad spectrum of substrates for peptides such as EA2, MucSAC, MucJA, M PubMed=12651884; DOI=10.1093/glycob/cwg062; Young W.W. Jr., Holcomb D.R., Ten Hagen K.G., Tabak L.A.; "Expression of UDP-GalNAc.polypeptide Nroc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). Event=Alternative splicing; Named isoforms=2; IsoId=Q6PB93-1; Sequence=Displayed; secreted form also exists. ALTERNATIVE PRODUCTS: and mouse cDNA sequences." IISSUE SPECIFICITY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricin B-type lectin.
Not glycosylated (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
MRRRSRMLLCFALLWVIGJAYYMYSGGGSALAAGGGGAGRK
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAHS9918;
0.2-WAR-2004 (TrEMBLrel. 27, Created)
0.2-WAR-2004 (TrEMBLrel. 27, Last sequence update)
0.2-WAR-2004 (TrEMBLrel. 27, Last annotation update)
0.2-WAR-2004 (TrEMBLrel. 27, Last annotation update)
UDP-N-acetyl-alpha-D-galactosamine:polypeptide
UDP-N-acetylagalactosaminyltransferase 2.
Mus musculus (Mouse)
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                  Polypeptide N-
acetylgalactosaminyltransferase 2,
acetylgalactosaminyltransferase 2,
soluble form.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Lumenal (Potential).
Catalytic subdomain A.
Catalytic subdomain B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.4%; Score 128.5; DB 1; Length 570; illarity 55.6%; Pred. No. 7.1e-09; Conservative 6; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGGRMEDIPCSRVGHIYRKYVPYKVP--AGVSLARNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / MALHNPQ (in isoform 2).
/FTIG-VSD 011201.
R - L (in Ref. 1).
C -> Y (in Ref. 2).
DSR -> NSK (in Ref. 1).
F -> V (in Ref. 1).
F -> V (in Ref. 1).
W, 90D5DC02C85A8EEA CRC64;
subfamily.
-!- SIMILARITY: Contains 1 ricin B-type lectin domain.
                                                                                                                                                                                                                                                                                                                             similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF348968; AAK37548.1; -.
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                                                                                                                                                                                                                                                                                                                                         570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                          51
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                   FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                            OMAIN
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AAH59818
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
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J. Cell Sci. 111:45-60(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9394011
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             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROWN.A.

STRAIN-C57BL/6; TISSUE-Brain;

MEDLINE=2238825; PubMed=1247932;

MEDLINE=238825; PubMed=1247932;

MEDLINE=238825; PubMed=1247932;

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zebebrg B., Buetow K.H., Schaefer C.P., Blata N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hableh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaddo M.P., Casavant T.L., Scheez T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochhynki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakernan R.J., Malek J.M., Gabes R.A.,

A Richards S., Worley K.C., Hale S., Garries A.M., Gabs R.A.,

A Richards S., Worley K.C., Hale S., Garries S., Sanchez A.,

A Rabes J., Halton B.K., Ketreman M., Madan A., Caibbs R.A.,

Rabes J., Halton B.K., Cormutz J., Myers R.M., Butterfield Y.S.,

Multing M., Madan A., Young A.C., Shevichenko Y., Boulfard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   010471; 03NDY4; 07NDY4; 07NDY4; 07NDY4; 07NDY4; 010672-2004 (Rel. 45, Last sequence update) 01-0CT-2004 (Rel. 45, Last sequence update) 01-0CT-2004 (Rel. 45, Last annotation update) 01-0CT-2004 (Rel. 45, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Gastric carcinoma;
MatbliNE-56025800; PubMed=7592619;
White T., Bennett E.P., Paul E., Takio K., Sorensen T., Bonding N.,
Clausen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and cDNA cloning of a human UDP-GalNAC; polypeptide N-
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      т
т
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.4%; Score 128.5; DB 2; Length 570; Best Local Similarity 55.6%; Pred. No. 7.1e-09; Matches 25; Conservative 6; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 CGGSLEIIPCSRVGHVFRKQHPYTFPGGSGTVFARNTRRAAEVWM 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC059818; AAH59818.1; -. Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGGRMEDIPCSRVGHIYRKYVPYKVP--AGVSLARNLKRVAD-WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570 AA; 64514 MW; 90D5DC02C85A8EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acetylgalactosaminyltransferase.";
J. Biol. Chem. 270:24156-24165(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse
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RESULT 12
GLT2 HUMAN
AC Q104714
DT Q1-0CTDT 01-0CTDE CAINAC
DE GAINAC
DE

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TISSUE-1ymph.

RX MEDLINE-2238657; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L.; Feingold E.A.; Grouse L.H. Derge J.G.

RA Alteschul S.F.; Zeeberg B., Bagner L.; Schaefer C.F.; Bhat N.K.;

RA Altschul S.F.; Zeeberg B., Bactow K.H.; Schaefer C.F.; Bhat N.K.;

RA Hopkins R.F.; Jordan H., Moore T., Max S.I.; Wang J., Hsieh F.,

RA Bitchenko L., Marusina K., Farmer A.A.; Rubin G.M.; Hong L.,

RA Brownstein M.J.; Usdin T.B.; Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A.; Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Rahay J., Helton E., Ketteman M., Madan A., Rokrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N. Kzzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human and manse constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: There are two conserved domains in the glycosyltransferase region: the N-terminal domain (domain A, also called GT1 motif), which is probably involved in manganese coordination and substrate binding and the C-terminal domain (domain B, also called Gal/GalNAc-T motif), which is probably involved in catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9295285;
Wandall H.H., Hassan H., Mirgorodskaya E., Kristensen A.K.,
Roepstorff F., Bennett E.P., Nielsen P.A., Hollingsworth M.A.,
Burchell J., Taylor-Papadimitriou J., Clausen H.,
"Substrate specificities of three members of the human UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosamine:polypeptide N-acetylgalactosaminyltransferase
[Emily, GalNAc-T1, -T2, and -T3.",
J. Biol. Chem. 272:23503-23514(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roctiger S., White J., Wandall H.H., Olivo J.-C., Stark A., Bennett B.P., Whitehouse C., Berger B.G., Clausen H., Nilsson T., "Localization of three human polypeptide GalNAc-transferases in HeLa cells suggests initiation of O-linked glycosylation throughout the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Golgi; resides
the Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UDP + N-acetyl-D-galactosaminyl-polypeptide. COFACTOR: Manganese and calcium (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type II membrane protein. preferentially in the trans and medial parts of secreted form also exists.
TISSUE SPECIFICITY: Widely expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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AAS64620
                                  Q7QDR0
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AAS64620
          RESULT 13
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                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way wouldied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    Calcium; Direct protein sequencing; Glycosyltransferase; Golgi stack;
Lectin; Manganese; Polymorphism; Signal-anchor; Transferase;
reaction and UDP-Gal binding (By similarity).
--- DOMAIN: The ricin B-type lectin domain binds to GalNAc and contributes to the glycopeptide specificity (By similarity).
--- SIMILARITY: Belongs to the glycosyltransferase family 2. GalNAc-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                portypeticus was acceptional acception of the form.

Cytoplasmic (Potential).

Signal-anchor for type II membrane protein (Potential).

Catalytic subdomain A.

Catalytic subdomain B.

Ricin B-type lectin.

Not glycosylated (Probable).

By similarity.

V. -> M (in Mobs. 2273970).

//FITIGANE 019575.

W. -> M (in Ref. 1; AA sequence).

R. -> G (in Ref. 1; AA sequence).

R. -> A (in Ref. 1; AA sequence).

H. -> M (in Ref. 1; AA sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Removed in soluble polypeptide N-acetylgalactosaminyltransferase 2. Polypeptide N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.4%; Score 128.5; DB 1; Length 571; llarity 55.6%; Pred. No. 7.1e-09; Conservative 6; Mismatches 11; Indels 3:
                                                   subfamily.
-!- SIMILARITY: Contains 1 ricin B-type lectin domain.
                                                                                                                                                                                                EMBL; AL078646; CACO0585.1; -
EMBL; AL136988 -; NOT ANNOTATED CDS.
EMBL; AL117349; -; NOT ANNOTATED CDS.
EMBL; BC041120; AAH41120.1; -.
HKS.P; P26514; IKNM.
Genew; HGNC:4124; GALNT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64732 MW;
                                                                                                                                                                                    EMBL; X85019; CAA59381.1; -.
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2210
2310
2310
232
522
533
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533
571 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 25;
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CONFLICT
CONFLICT
CONFLICT
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CONFLICT
CONFLICT
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TRANSMEM
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DISULFID
DISULFID
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DOMAIN
DOMAIN
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MEDLINE=20196006; PubMed=10731132;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Amanatides P.G., Scherer S.B., Li P.W., Hookins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortenan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfelifer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Man K.H., Boyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Baun A., Burck J., Broaktardin D., Bolshakov S.,
Burtis K.C., Bueam D.A., Buller H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Ade Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
N. Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                  AgCF10665 (Fragment).
AgCP10665 (Fragment).
Anopheles gamblae str. PEST.
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neophera; Endopherygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                      Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EWBL/GenBank/DDBJ databases.
-- CAUTION: The Sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/AAB01008849; EAA07231.1; -.
InterPro; IPR001173; Glycotrans.2.
InterPro; IPR001772; Ricin Blectin.
Pfam; PF00552; Ricin Blectin.
Pfam; PF00552; Ricin Blectin, 4.
PROSTIE; PS50231; RICIN BLECTIN; 2.
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9
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Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota;
Bukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; brosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS---LARNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 128; DB 2; Length 10
Pred. No. 1.5e-08;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1003 AA; 115923 MW; 753EA50F567A4E13 CRC64;
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01.APR-2004 (TrEMBLrel. 27, Last sequence update)
01.APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                 Last sequence update)
Last annotation update)
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                                                Created)
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Best Local Similarity 58.7%;
Matches 27; Conservative
                                             01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 STRAIN=PEST
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SEQUENCE
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2

Gaps

3

Similarity

1 CGGRMEDIPCSRVGHIYRKYVPYKVP--AGVSLARNLKRVAD-WM 42

345

g

3,

368 CGGSLEIIPCSRVGHVFRKRHPYTFPGGSGNVFARNTRRAAEVWM 412

RESULT 15

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AAQ56700

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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

A Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeeyam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lei Y., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Melson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

Reinert K., Remington K., Saunders R.D., Scheeler F., Shith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,

Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Khe B.C., Saveri J.S., Zhan M., Zhou K., Zho S., Zhu X., Smith H.O.,

A Cheng X.H., Myers E.W., Rubin G.M., Venter J.C.,

The genome sequence of Drosophila melanogaster.",

Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Frinshing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronniller B., Carlson J., Svirskas R.,
Tarise J.S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.5%; Score 126.5; DB 2; Length 590; 55.6%; Pred. No. 1.4e-08; tive 5; Mismatches 12; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003580; AAS64620.1; -.
SEQUENCE 590 AA; 65543 MW; 4E25C39CC3A9F3D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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PubMed=12829714;
Ten Hagen K.G., Tran D.T., Gerken T.A., Stein D.S., Zhang Z.;
Ten Hagen K.G., Tran D.T., Gerken T.A., Stein D.S., Zhang Z.;
Ten Hagen K.G., Tran D.T., Gerken T.A., Stein D.S., Denograter of the "Punctional Characterization and Expression Analysis of Members of the "DD-GalNAc: Polypeptide N-detylgalactosaminyltransferase Family from Drosophila melanogaster.",
J. Biol. Chem. 278:35039-35048 (2003).

EMBL, AY268064, AA265700.1, ...

Glycosyltransferase; Transferase.

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                                                                                                                         Drosophila melanogaster (Fruit fly).
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Bukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.5%; Score 126.5; DB 2; Length 615; 55.6%; Pred. No. 1.4e-08; ive 5; Mismatches 12; Indels 3;
                                   02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (EC
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Search completed: November 10, 2004, 13:38:31 Job time : 52.285 secs

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Local Similarity

1 CGGRMEDIPCSRVGHIYRKYVPXKVPAGVS--LARNLKRVAD-WM 42

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Gaps

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NESCUENCE 22-991A-33025

Sequence 33025, Application US/09252991A

Sequence 33025, Application US/09252991A

Sequence 33025, Application US/09252991A

Patent No. 6581795

GENERAL INFORMATION:

APPLICANTON:

TITLE OF INVENTION:

TITLE OF INV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appli
Sequence 33025, A
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Sequence 16, Appl
Sequence 20, Appl
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Query Match 26.6%; Score 54; DB 4; Length 106; Best Local Similarity 61.1%; Pred. No. 1.3; Matches 11; Conservative 3; Mismatches 4; Indels

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Sequence 2. Application US/09084303B

| Sequence 2. Application US/09084303B
| Patent No. 6627746
| GENERAL INFORMATION:
| APPLICANT: Reddy, Baindu
| APPLICANT: Reddy Baindu
| APPLICANT: Patent
| APPLICANT: Pragueon, Kimberly
| TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AND US
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                         US-09-759-875-8

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US-09-252-991A-29806

US-09-270-767-5615

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US-09-270-767-50650

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US-09-270-971-17379

US-09-252-991A-17379

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ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32986
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                                                                                                                                                                                                                                                                                                        Sequence 25877, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25877
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                  DB 4; Length 416;
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                                                                  Score 53; DB 4
Pred. No. 9.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 ALFHVDLDPGLDHFLGDFRLAPGEADLHH 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8529, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
                                                                                                                                                                                                  254 RRRAGSLPĽSRRVAĽCAHP 272
                                                                                                                                                          19 RRTPGDLHLDHSVHLCAHP 37
, ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8529
                                                                Query Match 26.1%;
Best Local Similarity 57.9%;
Matches 11; Conservative
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RESULT 5

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Sequence 6373, Application US/09128352
Sequence 6737, Application US/09128352
Patent No. 656298
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC99-0358
TURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6373
LENGTH: 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32986, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: MAKE J. Rubenfield et al.

APPLICANT: MAKE J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS:

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT ELLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR SEQ ID NOS: 33142

SEQ ID NO 32986

LENGTH: 575
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APPLICANT: Tukuo, Fukuda
APPLICANT: Tukuo, Fukuda
APPLICANT: Tukuo, Fukuda
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan E.
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: Ocnocaltions, and Methods for Control of Invertebrates
FILE REFERENCE: 21042.0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 LSWIAVQTBAB--ABRPRKRLGARPECVSVTGSIKFDLRIDPQLPLAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LSWIEMDTEMEMLLARFRRTPG------DLHLDHSVHLCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124.1%; Score 49; DB 4; Length 1297; 121rity 37.0%; Pred. No. 1.4e+02; Conservative 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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CURRENT FILING DATE: 1999-06-30
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Patent No. 6521454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Acinetobacter baumannii
US-09-328-352-6373
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GENERAL INFORMATION:

GAPLIANT KEITH WEINSTOKE et al

TITLE OF INVENTION: ROLD DIAGNOSTICS AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 20015

LENGTH: 653
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FALCENT HONDURGE Et al.
APPLICANT HONDURGE Et al.
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT FILINO NUMBER: US/09/270,767
CURRENT FILINO DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 36931
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ### Sequence 52148
| Sequence 52148 | Application US/09270767 |
| Sequence 52148 | Application US/09270767 |
| Patent No. 6703491 |
| GENERAL INFORMATION: |
| APPLICATY: Homburger et al. |
| TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster |
| TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster |
| CURRENT PAPLICATION NUMBER: US/09/270,767 |
| CURRENT FILING DATE: 1999-03-17 |
| NUMBER OF SEQ ID NOS: 62517 |
| SEQ ID NO 52148 |
| LENGTH: 66 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

23.4%; Score 47.5; DB 4;
Best Local Similarity 38.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 SLGW---ETEEICLNESFRLTPENLHISNWV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 RHGPNSWYLDGGLRLCSHHSYHOCTHP 58
Sequence 20015, Application US/09248796A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . TYPE: PRT
, ORGANISM: Drosophila melanogaster
US-09-270-767-36931
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US-09-270-767-52148
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Candida albicans
US-09-248-796A-20015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
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Matches 10; Conserv
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US-09-270-767-36931
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Sequence 2068, Application US/09540236

Sequence 2068, Application US/09540236

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT PILING DATE: 2000-04-04

CURRENT PILING DATE: 2000-04-04

SEQ ID NOS: 3840

LENGTH: 288
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US-09-328-352-5230

Sequence 5230, Application US/09328352

Sequence 5230, Application US/09328352

GENERAL INFORMATION:

APPLICANT: GATY L. Beton et al.

APPLICANT: GATY L. Beton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER;

TITLE OF INVENTION: BAUVANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILLE REFRENCE: GTOS9-03P8: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LENGTH: 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 353;
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Pred. No. 43;
                                                                                                                                                                                     Score 48; DB 4;
Pred. No. 19;
3; Mismatches
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    NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 MLLARFRRTPGDLHLDHSV 31
                                                                   ; LENGTH: 172
; TYPE: PRT
; ORGANISM: mosquito baculovirus
US-09-345-236B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.6%;
57.1%;
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23.6%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                           87 PNDIPLDHTIRLC 99
                                                                                                                                                                                                                                                                                 22 PGDLHLDHSVHLC 34
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Best Local Similarity
Matches 10; Conserv
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US-09-248-796A-20015
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US-09-540-236-2068
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; Sequence 12. Application US/09396149
; Sequence 12. Application US/09396149
; Patent No. 6538176
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVERTION: Maize Replication Protein A and Use;
; TITLE OF INVERTION: Maize Replication Protein A and Use;
; CURRENT APPLICATION NUMBER: US/09/396,149
; CURRENT PILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
23.2%; Score 47; DB 4; Length 273;
Best Local Similarity 30.8%; Pred. No. 45;
Matches 8; Conservative 6; Mismatches 12; Indels
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23.2%; Score 47; DB 4; Length 273;
Best Local Similarity 30.8%; Pred. No. 45;
Matches 8; Conservative 6; Mismatches 12; Indels
23.2%; Score 47; DB 4; Length 66; 37.0%; Pred. No. 8.5; Live 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09396149
Fatent No. 6538176
GENERAL INFORMATION:
FAPPLICANT: Mahajan, Pramod B.
TITLE OF INVENTION: Maize Replication Protein A and Use
FILE REPERENCE: 5718-59
CURRENT APPLICATION NUMBER: US/09/396,149
CURRENT APPLICATION NUMBER: US/09/396,149
CURRENT APPLICATION NUMBER: 1999-09-15
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 14
LENGTH: 273
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Patent No. 6538176
GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
TITLE OF INVENTION: Maize Replication Protein A and Use
PILE REFERENCE: 5718-59
CURRENT APPLICATION NUMBER: US/09/396,149
                                                                                                19 RRTPGDLHLD-----HSVHLCAHP 37
                                                                                                                                        32 RHGPNSWYLDGGLRLCSHHSYHQCTHP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 DIDLHTQVLNFFNEPANLESEHGVHV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 DTDLHTQVLNFFNEPANLESEHGVHV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 DTEMEMLLARFRRTPGDLHLDHSVHL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 DIEMEMLLARFRRIPGDLHLDHSVHL 33
                         Local Similarity 37.0
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Zea mays
US-09-396-149-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT

ORGANISM: Zea mays

US-09-396-149-14
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  Query Match
                           Best Loca
Matches
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; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 273
; TYPE: RT
; ORGANISM: Zea mays
US-09-396-149-16
Query Match
Best Local Similarity 30.8*; Pred. No. 45;
Matches 8; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
QY 8 DTEMEMLARFRRTPGDLHLDHSVHL 33

Qy 8 DTEMEMLARFRRTPGDLHLDHSVHL 33
Db 208 DTDLHTQVLNFFREFANLESEHGVHV 233
Search completed: November 10, 2004, 13:44:05
Job time: 12.7807 secs
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Fri Nov 12 14:55:15 2004
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November 10, 2004, 16:36:12 ; Search time 39.7478 Seconds (without alignments) 328.807 Million cell updates/sec
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| cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USIOA PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USIOA PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USIOA PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USIOA PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USIOD PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                   203
1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCAHP 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                          US-10-092-750-33
                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

u.	Sequence 33, Appl Sequence 137905, Sequence 167475, Sequence 122236, Sequence 1167473, Sequence 118, Appl Sequence 2412, Appl Sequence 14186, Sequence 167136, Sequence 167136, Sequence 350053, Sequence 350053,	
Description	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	
ΩΙ	US-10-092-750-33 US-10-425-115-357905 US-10-437-963-167475 US-10-437-963-122236 US-09-205-658-118 US-09-963-693-118 US-09-963-693-118 US-10-437-963-128 US-10-437-963-128 US-10-437-963-104186 US-10-437-963-104186 US-10-424-599-157136 US-10-424-599-157136 US-10-424-599-157136 US-10-424-599-157136	
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	equence equence equence	equence	2340 23559 66059 7766 24153	Sequence 262820, Sequence 1015, Ap Sequence 1015, Ap Sequence 101, Appl Sequence 207381, Sequence 83033, Sequence 188044, Sequence 3948, Sequence 37539, A Sequence 37539, A
US-09-764-847- US-10-092-154 US-10-425-114 US-10-425-1157	4 US-10-150-701-015 5 US-10-264-237-251 US-09-893-737-46 T US-10-455-115-263	1 US-09-864-408A-789 7 US-10-425-115-3398 5 US-10-424-599-1500 7 US-10-425-115-3398 6 US-10-425-115-3398 6 US-10-425-115-3398	4 US-10-043-467-29 5 US-10-424-599-22405 5 US-10-425-114-66059 6 US-10-425-114-66059 6 US-10-425-12086 4 US-10-424-599-24153	0 05-10-425-115-2 0 05-09-925-299-10 0 05-09-925-299-10 4 05-10-307-928A- 6 05-10-425-115-2 6 05-10-425-115-1 6 05-10-425-115-1 6 05-10-425-115-1 6 05-10-425-115-1 6 05-10-425-115-1 6 05-10-425-114-3
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# 10 10 10	200404	J 41 TV 70 L 80	20 U U W 4* N	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

ALIGNMENTS

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Gaps
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  Sequence 33, Application US/10092750
; bedication No. US2003003157A1
; bublication No. US2003003157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: POLYPEPTIGES Interactive with BCL-X1
; FILE REPRENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT APPLICATION NUMBER: US/60/274,526
; PRIOR PILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FRASESEQ for Windows Version 4.0
; SEQ ID NO 33
; LEMTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCAHP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-092-750-33
US-10-092-750-33
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1 ALSWIEMDTEMEMILARFRRTPGDIALDHSVHLCAHP 37 Sequence 357905, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION: RESULT 2 US-10-425-115-357905 g

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APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 122236
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ear Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Www. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bribaruk, Bric Mucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(3321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 167473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Clone ID: PAT_MRT4530_25183C.1.pep
US-10-437-963-122236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_66081C.1.pep
US-10-437-963-167473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.3%; Score 55.5; DB 16; Best Local Similarity 43.8%; Pred. No. 10; Matches 14; Conservative 4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 27.3%; Score 55.5; DB 16; Best Local Similarity 46.9%; Pred. No. 66; Matches 15; Conservative 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 IEMD-QVAMAIDR----PIDRHLHHQLRTCAH 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 167473, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 118, Application US/09205658; Patent No. US20010029617a1; GENERAL INFORMATION: APPLICANT: Runkun, Gary APPLICANT: Ogg, Scott
             Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-437-963-167473
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Wu, wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Bring Barbazuk, Brad
APPLICANT: Bring Barbazuk, Brad
APPLICANT: APPLICANT: APING Blants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
TITLE OF INVENTION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 167475
LENGTH: 1703
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Cao, Yinda
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REPERBNCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
KURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 357905
LENGTH: 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.5%; Score 62; DB 17; Length 141; Best Local Similarity 37.8%; Pred. No. 0.7; Matches 14; Conservative 5; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_66083C.1.pep
US-10-437-963-167475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCAHP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , CTHER INFORMATION: Clone ID: MRT4577_8957C.1.pep
US-10-425-115-357905
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: (1)..(141)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 EMEMLLARFRRIPG----DLHLDHSVHLCAH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 167475, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-10-437-963-122236
; Sequence 122236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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0
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; Publication No. US20030181364A1
; Publication No. US20030181364A1
; GENBRAL INFORMATION:
; APPLICANT: Ruvkun, Gary
APPLICANT: Gog, Scott
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; TITLE OF INVENTION: IMPAIRE: US/09/263,693
; CURRENT PILING DATE: 12001-09-25
; PRIOR FILING DATE: 1998-12-05-15
; PRIOR APPLICATION NUMBER: US/08/888,534
; PRIOR PELLING DATE: 1997-07-07
; PRIOR PELLING DATE: 1997-07-07
; PRIOR FILING DATE: 1997-07-07
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PASISEQ FOR Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.6%; Score 54; DB 10; Length 106; Best Local Similarity 61.1%; Pred. No. 7.6; Matches 11; Conservative 3; Mismatches 4; Indels
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS FILE REFERENCE: 00786/331004
CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
BARLIER APPLICATION NUMBER: 08/857,076
BARLIER APPLICATION NUMBER: 08/88,534
BARLIER APPLICATION NUMBER: 08/88,534
BARLIER PILING DATE: 1997-07-07
BARLIER APPLICATION NUMBER: US/09/0080
BARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTMARE: FSELSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 9; Length 106; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Caenorhabditis elegans US-09-963-693-118
                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Caenorhabditis elegans US-09-205-658-118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-09-963-693-118
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 118
LENGTH: 106
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TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AND USTILE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AND USTILE OF INVENTION: THEREOF.

FILE REPERENCE: 7326-069-999

CURRENT PELLING UNBERS: US/10/339,740

CURRENT PELLING DATE: 203-01-09

PRIOR PILING DATE: 1998-05-26

NUMBER OF SEQ ID NOS: 298

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 2

LENGTH: 106

TYPE: PRI

CREANISM: Caenorhabditis elegans

US-10-339-740-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Incorning Applicant: Leach, Martin D. APPLICANT: Shimkets, Richard A. TITLE OF INVENTION: No. US20040009474Alel Human Polynuclectides and Polypeptides EncorFILE REFERENCE: 21402-012 CURRENT APPLICATION NUMBER: US/09/864,408A CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: 60/206,690 PRIOR FILING DATE: 2000-05-24 NUMBER OF SEQ ID NOS: 9068 SOFTWARS: FastSEQ for Windows Version 4.0 SEQ ID NO 5412 LENGTH: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQUENCE 104186, Application US/10437963
SUGUENCE 104186, Application US/10437963
SUBLICATION TO US20040123343A1
GENERAL INFORMATION:
APPLICANT: APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Go, Yongwei
APPLICANT: W. Nei
APPLICANT: Barbauk, Brad
APPLICANT: Li, Piants and Uses Thereof for Plant Improvement .
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
26.6%; Score 54; DB 14; Length 106;
Best Local Similarity 61.1%; Pred. No. 7.6;
Matches 11; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SW-----IEMDTE-MEMLLARFRRTPGDLHLDHSVHLCAHP 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-864-408A-5412
; Sequence 5412, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-5412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-10-437-963-104186
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 ($2.02.1)
FILE OF DATE: 2003-02-28
CURRENT APPLICATION NUMBER: US (6)360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NOS: 47374
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.1%; Score 53; DB 14; Length 338;
Best Local Similarity 25.0%; Pred. No. 39;
Matches 13; Conservative 6; Mismatches 11; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Patent No. US200020132767A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITIE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITIE OF INVENTION NUMBER: US/09/764,847

CURRENT APPLICATION NUMBER: US/09/764,847

CURRENT APPLICATION NUMBER: US/09/764,847

NUMBER OF SEQ ID NOS: 2003

NUMBER OF SEQ ID NOS: 2003

SOFTWARE: PatentIn Ver: 2.0

SEQ ID NO 727

LENGTH: 51
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     DB 17; Length 59,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(338)

COTATER INFORMATION: unsure at all Xaa locations
US-10-369-493-3101
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                                                   3; Mismatches
  Query Match
26.1%; Score 53; D
Best Local Similarity 52.4%; Pred. No. 5.
Matches 11; Conservative 3; Mismatche
                                                                                                                                                                                                                                                                                 Sequence 3101, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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                                                                                                                                        21 TPGDLHLDHSVH----LCAHP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-764-847-727
                                                                                                                                                                                                                                   RESULT 13
US-10-369-493-3101
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US-09-764-847-727
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APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: En Rosa Thura
APPLICANT: Should K
APPLICANT: Con Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 138-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Anou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 [3322] B.
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 350053
LENGTH: 59
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8
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                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_101544C.1.pep
US-10-437-963-104186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; CTHER INFORMATION: Clone ID: PAT_MRT3847_112915C.1.pep
US-10-424-599-157136
                                                                                                                                                                                                                                Query Match 26.4%; Score 53.5; DB 16; Best Local Similarity 45.2%; Pred. No. 1.7e+02; Matches 14; Conservative 3; Mismatches 9;
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US-10-425-115-350053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LFWIIMDTHFECLLSSI-----LDYWLGLCA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCA 35
                                                                                                                                                                                                                                                                                                                                                                      474 EQHRLLARITRTPGRLYVVDDINLARPVYLMA 504
                                                                                                                                                                                                                                                                                                                                        10 EMEMLLARFRRIPG----DLHLDHSVHLCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 157136, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 350053, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104186
LENGTH: 1431
                                                                         TYPE: PRT
ORGANISM: Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-10-424-599-157136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-425-115-350053
                                                                                                                                FEATURE:
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Search completed: November 11, 2004, 01:28:15 Job time : 40.7978 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 8.24352 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

Title: Perfect score:

US-10-092-750-33 203 1 ALSWIEMDTEMEMLLARPRRTPGDLHLDHSVHLCAHP 37

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	cytochrome caa3 ox	cal pro	acp-22 protein - y	otein -	hypothetical prote	probable ATP /GTP-	proteins involved	protein involved i	0	hypothetical prote	hypothetical prote	_	glucose-1-phosphat	transcription fact	hypothetical prote	probable glycosyl	cellobiose oxidase	hypothetical prote	alpha-methyldopa-h	hypothetical prote	hypothetical prote	hypothetical prote	DNA-packaging prot	terminase large su	a)	-	SREBP cleavage act	Na+/H+ antiporter	hypothetical prote
SUMMARIES			ជា	G83976	T22615	S16063	S32224	T27989	T35469	AF1372	AD1742	C45335	E36792	T51959	S26845	E69392	C55973	A71347	D83472	860676	T29819	A28569	F85095	T49577	C82508	BPA	~		$\overline{}$	~	C83814	•
			DB	7	7	7	0	7	N	~	~	N	~	(7)	~	~	н	N	0	~	Ŋ	~	N	N	Ŋ	Н						
			Match Length	348	1270	199	199	106	886	159	159	342	599	141	211	241	363	448	494	770	343	464	513	604	242	641	641	641	641	1276	158	167
	de.	Query	Match	١,6	27.3	7	7	ė	ď.	25.6	'n.	ď.	ω.	25.4	S	S	25.1	S.	25.1	25.1	4.	4	24.6	4.	24.4	4.	24.4	24.4	4	24.4	₹	24.1
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		Result	No.	,	7	М	4	ഹ	φ	7	œ	δ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Apportetical protein T01E8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Cact-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22615; T24303
R;McMurray, A.
submitted to the EMBL Data Library, March 1995
A;Recession: T22615
A;Recession: T22615
A;Recession: T22615
A;Recession: T22615
A;Recession: T22615
A;Residues: DNA
A;Residues: L-1270 <WILL>
A;Residues: L-1270 <WILL>
A;Resperimental source: clone F54B3
R;McMurray, A.
R;McMurray, A.
A;Reperimental source: Clone F54B3
A;Reference number: Z19871

hypothetical prote	conserved hypothet	hypothetical prote	DnaJ-like protein	hypothetical prote	ATP-dependent heli	probable membrane	conserved hypothet	malonyl-CoA transa	3-deoxy-D-manno-oc	NADH2 dehydrogenas	hypothetical prote	interferon-induced	probable pdc prote	probable transcrip	DNA-directed RNA p
A97640	AB2863	T34406	T09338	867621	H83873	867053	G69158	T44805	E83023	T11515	T12515	A25407	E70814	C87128	865068
N	N	N	~	N	N	N	~	N	a	0	N	N	~	~	7
251	251	339	423	545	643	776	277	400	425	459	352	478	260	1106	1191
24.1	24.1	24.1	24.1	24.1	24.1	24.1	23.9	23.9	23.9	23.9	23.6	23.6	23.6	23.6	23.6
49	49	49	49	49	49	49	48.5	48.5	48.5	48.5	48	48	48	48	48
30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	4 7

ALIGNMENTS

G33976 G33976 G33976 G33976 Gytochrome caa3 oxidase (subunit II) ctaC [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: G83976 R;Accession: G83976 R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F; Hiran Nucleic Acida Res. 29, 4317-431, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c A;Reference number: A83650; MUDI:20512582; PMID:11058132 A;Accession: G83976 A;Ganerics: 1-348 cSTO-A A;Residues: 1-348 cSTO-A A;Residues: 1-348 cSTO-A A;Bacidues: 1-348 cSTO-A A;Experimental source: strain C-125 C;Genetics: C;Genetics: C;Genetics: A;Genetics: C;Genetics: C;Genetics	
Cytochrome caaj oxi CySpecies: Bacillus C;Accession: G83976 C;Accession: G83976 R;Takami, H; Nakas Nucleic Acids Res. A;Accession: G83976 A;Status: prelimina A;Molecule type: DN A;Residues: 1-348 A;Gross-references: A;Gross-references: A;Gross-references: A;Gross-references: A;Gene: CtaC C;Guperfamily: CytoC;Gsuperfamily: CytoC;Keywords: Chromop F;209,211,212,217/FF F;211,81nding site: F;217,181nding site: Cuery Match Best Local Simila	
C. Species Bacillus C. Sacession: G83976 R. Taxaan, H.; Nakas Nuoleic Acids Res Nuoleic Acids Res A. Title: Complete 9 A. Reference number: A. Scession: G83976 A. Setatus: prelimina A. Status: prelimina A. Gross-references: A. Residues: 1-348 A. Gross-references: A. Seperiamina C. Superfamily: cyto F. 209. 2117 F. 211 (Binding site: F. 267, 270/Binding site: Best Local Simila Matches I. S. Cocal Matches I. S. Cocal Matches I. S. Cocal Matches II. Samila	Cytochrome casa oxidase (subunit II) ctaC (imported) - Bacillus halodurans (strain C-125)
C. Accession: G83976 R.Takami, H.; Nakas N.Tucle: Acids Res. A.Reference number: A,Accession: G83976 A,Stesidue: prelimina A,Molecule Lype: DN A,Residues: 1-348 A,Esperimental Sour C,Genetics: C,Gen	s natoquians n #semience yessision 01-Dec-2000 #text absorp 00-1311-2004
R, Takami, H.; Nakaa Nuoleic Acids Res. A, Reference number: A, Accession: G83976 A, Status: prelimina A, Molecule type: DN A, Residues: 1-348 A, Residues: 1-348 C, Generics: A, Generics: A, Generics: 1 A, Generics: A, Generics: 1 A, Generics: A, Generics: 1 B, 1209, 211, 1213, 217/ F, 209, 211, 1213, 217/ F, 209, 211, 1213, 217/ F, 209, 211, Sinding site: F, 271, Sinding site: Guery Match Best Local Simila Matches 127, 270, 270, 270, 270, 270, 270, 270, 2	s sequence revision or becased sectoriange of our roots
Nucleic Acids Res. A.Title: Complete g A.Reference number: A.Accession: G83976 A.Residues: prelimina A.Residues: 1-348 A	sone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; I
A.Title: Complete 9 A.Reference number: A.Accession: G83976 A.Status: prelimina A.Molecule type: DN A.Residues: 1-348 A.Texperimental sour C.Genetics: A.Gene: ctaC C.Superfamily: cyto C.	Nucleic Acids Res. 28, 4317-4331, 2000
A, Reference number: A, Stactus: prelimina A, Status: prelimina A, Molecule type: DN A, Residues: 1-348 A, Greatus: 1-348 A, Greatus: 1-348 A, Greatus: 1-348 C, Superfamental sour C, C, Superfamily: cyto C, Super	A, Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c
A. Status: prelimina A. Molecule type: DN A. Molecule type: DN A. Kosidus: 1-348 A. Experimental sour C. Geneics: A. Gene: ctac C. Superfamily: cyto C. Keywords: chromop F. 209, 211, 213, 217, BF; 211, Binding site: F; 271/Binding site: F; 271/Binding site: Cuery Match Best Local Simila Matches 12; CO	: A83650; MUID:20512582; FMID:11058132
A; Modecule Type: DA; Modecule T	**************************************
A,Residues: 1-348 < A,Cross-references: A,Experimental sour C,Genetics: A,Gene: CtaC C,Superfamily: cytco C,Keywords: chromop P,209,211,213,217/B P,211/Binding site: F,271/Binding site: E,271/Binding site: E,271/Binding site: Best Local Simila Matches 12,717	7.1% RN
A Cross-references: A Experimental sour C Generics: A Gene: ctaC C Superfamily: cyto C	\S\TO\
A.Experimental sour Cenetics: A.Gene: ctac C.Superfamily: cyto C.Reywords: chromop F:209,211,211/Binding site: F:211/Binding site: F:271/Binding site: F:271/Binding site: F:271/Binding site: F:271/Binding site: B:271/Binding site: Matches Simila Matches 12;	A; Cross-references: UNIPROT: Q9K9N0; GB: AP001516; GB: BA000004; NID: 910175192; PIDN: BAB063:
C.Genetics: A.Gene: ctcC C.Superfamily: cyto C.Keywords: chromop P.209,211,213,217F F:211/Binding site: F:271/Binding site: F:271/Binding site: Guery Match Best Local Simila Matches 12,	rce: strain C-125
A,Gene: ctaC C,Superfamily: cyto C,Keywords: chromop F,209,211,213,217/B F,211/Binding site: F,271/Binding site: F,271/Binding site: Query Match Best Local Simila Matches 12.	
C.Superfamily: cyto C.Keywords: chromop F.209, 211, 213, 217/B F,211/Binding site: F,271/Binding site: F,271/Binding site: Ouery Match Best Local Simila Matches 12, 217	
C.Keywords: chromop F.209,211,213,217/B F.311/Binding site: F.267,270/Binding site: F,271/Binding site: Query Match Best Local Simila Matches 12,000	ochrome-c oxidase chain II, cytochrome c containing; cytochrome c6
F.209,211,213,21/B F.21/Bainding site: F.277,20/Binding site: F.271/Binding site: Query Match Best Local Simila Matches 12,	protein; copper; electron transfer; heme; iron; membrane-associated
F:211/Binding site: F:267,270/Binding site: Couery Match Best Local Simila Matches 12,	sinding site: copper 2 (Cys, Glu, Cys, His) #status predicted
F:267.270/Binding s F;271/Binding site: Query Match Best Local Simila Matches 12; Co	: magnesium (Glu) (shared with chain I) #status predicted
Query Match Best Local Simila Matches 12, Co	site: heme (Cys) (covalent) #status predicted . heme iron (His) (axial ligand) #status predicted
Query Mat Best Loca Matches	50001450144
Matches	29.0%
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APTITAL TO ATT	13 MILARPRITGELHIDHSVH 32
Db 66 IILAR	::

C, Genetics:

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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF1372
C;Accession: AF1372
C;Accession: AF1372
C;Accession: AF1372
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001
C;Date: 27-Nov-2001
D;Date: 27-Nov-2001

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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-886 cMUR>
A,Cross-references: UNIPROT:086768; EMBL:AL031035; PIDN:CAA19923.1; GSPDB:GN00070; SCOEDE
A,Experimental source: strain A3(2)
A,Gene: SCOEDB:SC6A9.38
A,Gene: SCOEDB:SC6A9.38
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                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT;Q09626; EMBL:U23451; PIDN:AAC46744.1; CESP:ZK75.1
A;Experimental source: strain Bristol N2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable ATP /GTP-binding protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35469
hypothetical protein ZK75.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1998
A; Reference number: Z21578
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C;Superfamily: Caenorhabditis elegans hypothetical protein ZK84.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.6%; Score 54; DB 2; Length 106; Best Local Similarity 61.1%; Pred. No. 2; Matches 11; Conservative 3; Mismatches 4; Indels
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Pred. No. 34;
2; Mismatches 10;
                                                                                                                                                                           Rikirsten, J. submitted to the EMBL Data Library, July 1995
A,Description: The sequence of C. elegans cosmid ZK75. A)Reference number: Z20451
A,Reference number: Z20451
A,Accession: T27989
                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-106 <KIR>
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36 IEMETELENQLSRARRVP 53
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ilarity 45.2%;
Conservative
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Best Local Similarity
Matches 14; Conserv
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A,Molecule type: DNA
A,Residues: 1-159 <GLA>
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                                                                                                                                                                                                                                                                                               A;Gene: CESP:T01E8.5
A;Map position: 2
A;Introns: 15/1; 35/3; 73/3; 99/2; 237/1; 277/3; 332/3; 397/2; 534/3; 703/3; 1006/1; 119
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                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1270 «WI2>
A;Coss-references: EMBL:248809; PIDN:CAA88749.1; GSPDB:GN00020; CESP:T01E8.5
A;Experimental source: clone T01E8
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C,Species: Tenebrio molitor (yellow mealworm)
C,Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acp-22 protein - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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A;Modecule type: DNA
A;Residues: 1-199 <BOU>
A;Cross-references: UNIPROT:P26968; EMBL:X72783; NID:9288439; PID:9288440
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R; Bouhin, H.; Charles, J.P.; Quennedey, B.; Delachambre, J.
Subnitted to the EMBL Data Library, July 1991
A; Description: Molecular cloning of a glycine-rich cuticular protein.
A; Reference number: S16063
A; Accession: S16063
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27.3%; Score 55.5; DB 2; Length 1270;
Best Local Similarity 41.9%; Pred. No. 19;
Matches 13; Conservative 7; Mismatches 8; Indels· 3.
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27.1%; Score 55; DB 2; Length 199;
Best Local Similarity 52.9%; Pred. No. 2.9;
Matches 9; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 199;
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R;Bouhin, H; Braquart, C.; Charles, J.P.; Delachambere, J. Bubmitted to the EMBL Data Library, March 1993
A;Reference number: S32224
A;Accession: S32224
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Pred. No. 2.9;
4; Mismatches
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626 ISWIEVEREMMNIDARVKRTKLKDCELYEDH 656
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TPVDVHHEEAIHLKAHP 134
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118 TPVDVHHEEAIHLKAHP 134
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ilarity 52.9%;
Conservative
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Best Local Similarity
Matches 9; Conserv
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A;Molecule type: mRNA
A;Residues: 1-199 <BOU>
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                                       A; Accession: T24303
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Genetics:

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C;Species: Picea mariana
C;Species: Picea mariana
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T51959
R;Perry, D.J; Bousquet, J.
Genetics 149, 1089-1098, 1998
A;Title: Sequence-tagged-site (STS) markers of arbitrary genes. Development, characterizations A;Reference number: Z25268; MUID:98278823; PMID:9611216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A,Residues: 1-599 <DAV>
A,Cross-references: UNIPROT:Q00157; GB:M75136; NID:g331209; PIDN:AAA88161.1; PID:g331268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: E36792
                                                                Gaps
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C;Species: ictalurid herpesvirus 1
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A;Cross-references: UNIPROT:065048; EMBL:AF051205; PIDN:AAC32110.1
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C,Superfamily: ictalurid herpesvirus 1 hypothetical protein ORF58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R,Davison, A.J. submitted to GenBank, January 1992 A;Description: Channel catfish virus: a new type of herpesvirus. A;Reference number: A36804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 599;
                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribavison, A.J.
Virology 186, 9-14, 1992
Virology 186, 9-14, 1992
Afitle: Channel catfish virus: a new type of herpesvirus. A;Reference number: A39447; MUID:92087490; PMID:1727613
A;Contents: annotation
                                                                . 9
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A;Molecule type: mRNA
                        45.0%; Pred. No. 14;
tive 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 WIKQDPAMAM----FRRYPIDLRLERMI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WIEMDTEMEMLLARFRRTPGDLHLDHSV 31
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                                                                                                                                    13 MLLARFRATPGDLHLDHSVH 32
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66 IILAKYRRKPGDDEIPKQVH 85
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Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dTMP kinase (EC 2.7.4.9) - human
                        Best Local Similarity 45.0
Matches 9; Conservative
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S26845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         process involved in resistance to cholate and to NA(+) and in pH homeostasis homolog ling (Species: Listeria innocua (C.Species: Listeria AD1742)

C.Accession: AD1742

E.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A; Multors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, Title: Comparative genomics of Listeria species.

A; Mitle: Comparative genomics of Listeria species.

A; Mccession: AD1742

A; M
A;Cross-references: UNIPROT:Q8Y4Q2; GB:NC_003210; PIDN:CAD00460.1; PID:g16411870; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2382
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
C45335
C45335
C45335
C5ytochrome-c oxidase (EC 1.9.3.1) chain II - Bacillus firmus
C;Species: Bacillus firmus
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accession: C45335; 139821
R;Quirk, P.G.; Hicks, D.B.; Krulwich, T.A.
J. Biol. Chem. 268, 678-685, 1993
A;Title: Cloning of the cta operon from alkaliphilic Bacillus firmus OF4 and characteriz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: Cytochrome-c oxidase chain II, cytochrome c containing, cytochrome-c oxid C;Reywords: copper; electron transfer; heme; membrane-associated complex; oxidoreductase C;Reywords: cytochrome-c oxidase chain II homology <CO2>
F;31-228/Domain: cytochrome-c oxidase chain II homology <CO2>
F;175,210,214,221,Binding site: copper I (His Cys, Cys, Mis) #status predicted F;210,212,214,218/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted F;212/Binding site: magnesium (Glu) (shared with chain I) #status predicted
                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M94110; NID:g142782; PIDN:AAA22364.1; PID:g142786
A;Experimental source: strain OF4
C;Genetics:
                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 2; Length 159;
Pred. No. 6.1;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                        Score 52; DB 2; Length 159;
Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: lin2481
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB1401
                                                                                                                                                                                                                                                                                                                                                                                                                                            5 IEMDTEMEMLLARFRRTPGDLHLD-----HSVHL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 IEMDTEMEMLLARFRRTPGDLHLD-----HSVHL 33
                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.6%; Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: strain Clip11262 C, Genetics:
                                                                                                                                                                                                                                Query Match
Best Local Similarity 33.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.6%;
Local Similarity 33.3%;
les 13; Conservative
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A;Map position: 2pter-2qter C;Superfamily: dTMP Kinase C;Keywords: nucleotide binding; P-loop; phosphotransferase F;13-20/Region: nucleotide-binding motif A (P-loop)

A; Cross-references: GDB:127511; OMIM:188345

A; Gene: GDB: DTYMK

A; Molecule type: mRNA A; Residues: 1-211 <SUJ>

2 LSWIEMDTEMEMLLARFRRTPGDLHLDHSVHL 33

RESULT 13

Local Similarity nes 13; Conserv

8 g

Query Match Best Loca Matches

> d à

1-241 <KLE>

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hypothetical protein TP0260 - syphilis spirochete
Cispecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
Cispecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
Cispecies: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
Ciscession: A71347
Schools: A. Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinr rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDor they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Schools: 1. Weidman, J.; Smith, H.O.; Venter, J.C.
Schools: J. 375-188, 1998
A. Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A. A. Title: Complete genome sequence of Treponema pallidum, translation not shown
A. Schools: L. 448 COLE.
A. Molecule type: DNA
A. Residues: 1-448 COLE.
A. Molecule type: DNA
A. Molecule 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AjGene: is1-3
C;Superfamily: transcription factor is1-1; homeobox homology; LIM metal-binding repeat ht C;Superfamily: transcription splicing; DNA binding; duplication; homeobox; nucleus; transcript F;27-80,Domain: LIM metal-binding repeat homology <LIM.>
F;89-142/Domain: LIM metal-binding repeat homology <LIM.>
F;89-148/Domain: homeobox homology <HOX>
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A,Experimental source: strain Nichols
R;Gong, Z.; Hew, C.L.
Biochim. Blogblys. Acta 1260, 349-354, 1995
A;Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchu
A;Reference number: S52089; MUID:95178560; PMID:7873614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 448;
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C;Superfamily: syphilis spirochete hypothetical protein TP0260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.1%; Score 51; DB 2;
40.0%; Pred. No. 26;
tive 5; Mismatches 11
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                                                                                                                                                                                                                                                                                                               <602×
                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-82, 'IMNKACKAMQPGIQQO'
A,Cross-references: EMBL.X64883
A,Note: alternative splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 40.7 nes 11; Conservative
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nes 12; Conserv
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
C55973

transcription factor isl-3 - chinook salmon
NAlternate names: insulin enhancer-binding protein isl-3; islet-3 protein
NyAlternate names: insulin enhancer-binding protein isl-3; islet-3 protein
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Species: Oncorhynchus tschamytscha (chinook salmon)
C;Species: Oncorhynchus tschamytscham (chinook salmon)
R;Gong, Z.; Hui, C.; Hew, C.L.
S; Biol., Chem. 270, 333-3345, 1995
A;Tile: Presence of isl-1-related LIM domain homeobox genes in teleost and their simila A;Reference number: ASS973; MUID:95155429; PMID:7852419
A;Residues: C55973
A;Residues: 1-363 cGON>
A;Residues: UNIPROT:P53409; GB:X64883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-241 «KLE»
A;Cross-references: UNIPROT:029123; GB:AE001025; GB:AE000782; NID:G2689348; PIDN:AAB901d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT: P23919; EMBL: X54729; NID: g37205; PIDN: CAA38528.1; PID: g37206
                                                                                        C;Accession: S26845
R;Su, J.Y.; Sclafani, R.A.
Nucleic Acids Res. 19, 823-827, 1991
A;Title: Molecular cloning and expression of the human deoxythymidylate kinase gene in A;Reference number: S26845; MUID:91204436; PMID:2017365
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
         N'Alternate names: deoxythymidylate kinase
C'Species: Homo sapiens (man)
C'Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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25.1%; Score 51; DB 2; Length 241;
Best Local Similarity 42.9%; Pred. No. 13;
Matches 9; Conservative 5; Mismatches 7; Indels
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GenCore version 5.1.6
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November 10, 2004, 12:27:34 ; Search time 45:1796 Seconds (without alignments) 471.205 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-092-750-33 203 1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCAHP 37

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	O7rd36 plasmodium	OBilal plasmodium	bac	orvza sat	78 Orvz	3 orvza sati	vibrio	vibrio			۵	caeno		· c	z ispo	O9xta0 equus cabal	aenor	nopheles	0991c6 rattus norv		rattus	Q89ex1 bradyrhizob	Q6mgs6 bdellovibri	Cae78371 bdellovib		Cae78453 bdellovib		9	ਗ	
	ć	TT.	Q7RQ36	OSILGI	0N6X6O	Q7FAB9	CAE03978	O7XEA3	O7MCN7	QBDSN2	Q8DHF7	69LH89	QBRYX8	020749	AC22 TENMO	<u>о</u> вки <u>м</u> з	ISDF ZYMMO	Q9XTÃ0	ILB1 CAEEL	Q7PX17	099JC6	AAH62007	CAE83920	Q89EX1	QEMQSE	CAE78371	Q6MQJ4	CAE78453	Q6N5Z5	CAE28265	Q9L169	
	ć	ה ה	~	~	7	~	N	Ä	~	7	~	~	ď	~	Н	~	Н	~	н	N	~	0	7	~	~	~	0	7	N	~	N	•
	1	Length	2156	2657	348	1479	1479	1708	422	422	658	428	559	1270	199	213	387	610	106	312	464	464	464	^	1061	0	557	557	96	96	486	4
de	Query	March	ď	32.8	o,	7.	۲.	•	27.6	۲.	7.	7.	7.	۲.	7.	26.8	ė.	ė.	ė.	9	Ġ	•	ė.	ė.	ý.	ė.	26.4	Ġ.		26.1		
	5	Score	ø.	ė.	9	ė	56.5	è.	56	26	26	'n.	55.5	ŝ	52	54.5	٠	4.	54	54	54	54	54	54	54	S	٠	m	53	53	ß	
	Result		7	N	m	4	Ŋ	v	7	80	o	10	11	12	13	14	15	16	17	18	9	20	21	22	23	24	25	26	27	28	9	

Aas71837 leptospir O86768 streptomyce	Q928q1 listeria in O8v4q2 listeria mo	Q71x44 listeria mo Aat05121 listeria	Q04441 bacillus ps	Q00157 ictalurid h O8sa69 viqna radia	O65048 picea maria		Q82pj0 streptomyce		Q6cam9 yarrowia li
AAS71837 086768	Q928Q1 Q8Y4Q2	Q71X44 AAT05121	COX2_BACPF	VG58 ICHV1 Q8SA69	065048	KTHY_HUMAN	Q82PJ0	Q7WR40	Q6CAM9
0.0	N N	0 0	Н.	H (1)	(1	-	~	~	N
659 886	159	159	342	669 609	141	212	376	403	140
25.9	25.6	25.6	25.6	25.6	25.4	25.4	25.4	25.4	25.1
52.5	5 2 2	N 22	25	2 22	51.5	51.5	51.5	51.5	21
33	3.34 3.5	36	38	6 4 0 0	41	42	43	44	45

ALIGNMENTS

RESULT Q7RQ36	1 2 0 0 0 0		ì		
a S	07R036	PRELIMINARY;	PRT; 2156 AA.		
님	01-MAR-2004		Created)		
텀	01-MAR-2004	(TrEMBLrel. 26,			
3 8			rast annotation update)		
N U	Name=PY01267				
ဗ		yoelii yoelii.			
88	Eukaryota; Alveol	lveolata; Apicor 2019:	Alveolata; Apicomplexa; Haemosporida; Plasmodium. 73239.		
Z.	[1]	-			
RЪ	SEQUENCE FROM	FROM N.A.			
2	STRAIN=17XNL;	•			
ž:	PubMed=12368865;	865;			
5 5	Silva T C	Angluoil S.V.,	Sun B.B., Koolj T.W., Pertea M.,		
5 2	Peterson J.D.	Pop M., Kosac	Stiva C.C., Eimolaeva M.D., Allen U.E., Selengur C.D., ACO H.D. Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,	•	
R.A	Shallom S.J.,	, van Aken S.E.,	Riedmuller S.B., Feldblyum T.V.,		
Æ.	Cho J.K., Que	ackenbush J., Se	Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.	۲.,	
8 2	Florens L.,	rates F.R. III,	R.E., Harris	M.A.,	
¥ 6	Cunningnam D.	Tango C. T. M.	Cunningnam D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,		
5 2	Salzberg S.L.	. Venter J.C.	teers A.F., Smith A.O., White O.K., Fraser C.M., Hoffman S.L., Gardner	Σ	
R.	Carucci D.J.;			:	
RI	"Genome sequence	ence and comparative	tive analysis of the model rodent	malaria	
R.	parasite Plas	parasite Plasmodium yoelii yoelii.";	roelii.";		
3 E	Nature 419:512-51	9 (2002)			
ខ្លួ		DDBJ whol	shotonn (WGS) entry which	ä	
ပ္ပ	preliminary	iry data.		1	
ä i	EMBL; AABL01(EMBL; AABL01000331; EAA20560.1;			
H 6	GO; GO:0003993;	33; Fracid phosphatase	hatase activity; IEA.		
ž 2	INCELPTO; LPR	property Hisac phapmase.	nsphise. Mosnam 1. 1		
íŽ	Hypothetical	protein	noskaki_i; i.		
SO	SEQUENCE 21	2156 AA; 249387 MW;	MW; 47FBCC1CA2236384 CRC64;		
S	/ Match		Score 66.5; DB 2; Length 2156;		
M Be	Simi 3;	Similarity 39.4%; .3; Conservative	No. 4.4; matches 13; Indels	Gaps	ų
à	3 SWIE	SWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCA	PGDLHLDHSVHLÇA 35		
		======================================			
d D	351 NWYS	NWYSIENBEBVÍRKTFRQ-ÞDDÍHCSHHEBLÖS	РОБЪНСЅНИВБЪСЅ 382		
RESULT Q8ILG1	8				
A D		PRELIMINARY;	PRT; 2657 AA.		
ם	2003	(TrEMBLrel. 23, (TrEMBLrel. 23,	Created) Last sequence update)		

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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=12447439;
                                                                                                                                                                                                                                                                                                                               Transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Q7FAB9
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THE ALGORIZAM A.17

THE ALGORIZAM A.16

THE ALGORIZAM A.16

THE ALGORIZAM A.16

THE ALGORIZAM A.17

THE AL
                                                                                                                                                                                                                 MEDLINEZ-225705; PubMed=12168864;
MEDLINEZ-225705; PubMed=12168864;
MEDLINEZ-225705; PubMed=12168864;
MEDLINEZ-225705; PubMed=12168864;
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallon S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlanda A.H., Fraunholz M.J., Roos D.S., Ralph S.A., NcFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.8%; Score 66.5; DB 2; Length 2657; 39.4%; Pred. No. 5.5;
                                         ORFNames=PF14_0285;...
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
VOBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus halodurans.
Bacteria, Firmicutes; Bacillales; Bacillaceae, Bacillus.
NCBI_TaxID=86665;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome caa3 oxidase (Subunit II).
      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 419:498-511(2002).
EMBL, AE014820; AAN16895.1; -.
EGO, GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR000560; HisAc_phosphtse.
PROSTIT; PS00616; HIS_ACID_PHOSPHAT_1; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 NWYNIENBEEVLRKTFRQ-PDDLHCSHHEELCS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.4 Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Q9K9N0
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Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Luu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Nang R., Yin H.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang R.,
Wang L., Ding C., Sheog H., Chen S., Sun Y., Hu Q., Zhang X.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
InterPro; IPR002327; Cyt CIAB.
InterPro; IPR002429; Cyt_c_ox_2.
Pfam; PF0016; COX2_TM; 1.
Pfam; PF00034; Cytochrom C; 1.
PRINTS; PR01166; CYCXIDASEII.
ProDom; PD000131; Cytochrom C; 1.
ProDom; PD0001375; Cyt_CIAB; 1.
ProDom; PD0001375; Cyt_CIAB; 1.
PROSTIRS; PS000798; COXZ; 1.
PROSTIRS; PS00190; CYTOCHROME_C; UNKNOWN_1.
Electron transport; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Oryza stiva (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 348;
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SMART; SM00343; ZDF CZHC; 1.
PROSITE; PS50158; ZF CCHC; 1.
SEQUENCE 1479 AA; 162541 MW; 8A8E584CA2A33DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 348 AA; 38585 NW; EA287CD1AC9AE323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence and analysis of rice chromosome 4.";
"Sequence and analysis of rice chromosome 4.";
EMBL, AL662942; CAE03978.3; -.
Interpro; IPR001584; Rve.
Interpro; IPR0018975; Viral_cap_coat.
Interpro; IPR001878; Zif_CCHC.
Pfam; PF00665; rve; 1.
Pfam; PF00665; rve; 1.
Pfam; PF00065; zf-CCHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.8%; Score 56.5; DB 46.9%; Pred. No. 80; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   uery Match 29.6%; Score 60; DB 2 est Local Similarity 60.0%; Pred. No. 4.7; atches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 MLLARFRRTPGDLHLDHSVH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 ILLARFRRKPGDDELPKQVH 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
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Name=OSJNBa0033H08.2;
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Pfam; PF00651; BTB; 2.
Pfam; PF00655; rve; 1.
Pfam; PF00099; zf-CCHC;
SMART; SM00225; BTB; 1.
SMART; SM00343; znF-C2HC; 1.
PROSTTE; PS50097; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=14656965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=VVA1349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogen.";
Genome Res.
                                                                                                                                                                                                                      Polyprotein,
SEQUENCE 1
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Q8D5N2
ID Q8D5N
AC Q8D5N
DT 01-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Liu Y., Lu Y., Mu W., Lu Y., Zhang L., Lu Y., Mu W., Lu Y., Zhang L., Lu Y., Mu W., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Uin Z., Wang R., Yin H., Chen S., Ly G., Gu W., Zhu G., Tu Y., Jia J., Zhang R., Xho H., Shao G., Sun Y., Hu Q., Zhang X., Zhang W., Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Han B., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cuitivar-group).
Wkaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza; Oryza sativa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017096; AAF53887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATÚTE 420:316-320(2002).
EMBL; ALG62942; CAE03978.3; -.
SEQUENCE 1479 AA; 162541 MW; 8A8E584CA2A33DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                              Last sequence update)
Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence and analysis of rice chromosome 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 EMEMLLARFRETPG----DIHLDHSVHLCAH 36
                                     1479 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.8%; Score 56.5; D
46.9%; Pred. No. 80;
:ive 2; Mismatches
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                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
MEDLINE=22337377; PubMed=12447439;
                               CAE03978 PRELIMINARY;
CAE03978;
02-MAR-2004 (TYEMBLYEL) 27, CAE
02-MAR-2004 (TYEMBLYEL) 27, LG
02-MAR-2004 (TYEMBLYEL) 27, LG
02-NABA0033H08, 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative gag-pol polyprotein.
ORFNames=OSJNBa0073D04.30;
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Best Local Similarity 46.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=39947;
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CAE03978

AC CAE0 AC CAE0

DT CO-M
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                                                                                                   Gaps
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Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
"Comparative genome analysis of Vibrio vulnificus, a marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                Length 1708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio vulnificus (strain YJ016).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
VIBI_TaxID=196600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.6%; Score 56; DB 2; Length 422; 35.9%; Pred. No. 22; ive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP005349; BAC97375.1; -. ACO GO.0005524; F.ATP binding; IEA.

GO; GO.0003234; F.RATP binding; IEA.

GO; GO.0004831; F.RATP binding; IEA.

GO; GO.0004831; F.LYTOSING-LRNA ligase activity; IEA.

GO; GO.0004831; F.LYTOSING-LRNA ligase activity; IEA.

GO; GO.0004831; F.LYTOSING-LRNA aminoacylation; IEA.

InterPro; IPRO02345; SANA-SYNL ID.

InterPro; IPRO02305; LRNA-SYNL ID.

PEAM; PRO1479; A4; 1.

PROSTIF; PRO1409; TRNA-SYNL ID; 1.

PROSTIF; PSO1040; TRNA-SYNTHTR.

ITGREAMS; TIGREAMS; LLYS; 1.

PROSITE; PSO178; AA_TRNA_LIGASE_I; 1.

RESOITE; PSO178; AA_TRNA_LIGASE_I; 1.

RESOITE; PSO3899; S4; 1.

RAMINOACYL-LRNA SYNTHELSSE.

SEQUENCE 422 AA; 47161 NW; OAC47AC4DBA654F5 CRC64;
                                                                                                 10; Indels
OBODE550A15A746E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         16 IAQTTDLEQLIALFRQPQTLYCGFDPTAGSLHIGHLVPL
                                                   DB 2;
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                                                                                                                                                    10 EMEMLLARFRRTPG-----DLHLDHSVHLCAH 36
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                                                Query Match
27.8%; Score 56.5; Dest Local Similarity 46.9%; Pred. No. 94; Matches 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                 422
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  1708 AA; 188208 MW;
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Q8D5N2;
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
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QBRYX8;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
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SEQUENCE FROM N.A.
MEDLINE=20363099; PubMed=10907853;
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Best Local Similarity 27.58
Matches 11; Conservative
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DNA Res. 7:217-221(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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ID O8
AC O8
DT 01
DT 01
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DNA Res. 9:123-130(2002)

-1 - SINILARITY: Belongs to the ABC transporter family.

EMB1, AP005375; BAC09554.1; -. .

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005509; F:ATP binding; Lassette (ABC) transporter acti. . .; IEA.

GO; GO:0015112; F:nitrate transporter activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                             Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. VCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 422;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016811; AAO07799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aminoacyl-tRNA synthetass; Complete proteome.
SEQUENCE 422 AA; 47173 MM; 0C65F0586119F26B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005524; F:ATP binding; IBA.
GO; GO:0005523; F:RNB binding; IBA.
GO; GO:0003723; F:RNB binding; IBA.
GO; GO:0004831; F:tyrosine-tRNA ligase activity; IBA.
GO; GO:0006437; P:tyrosyl-tRNA aminoacylation; IBA.
InterPro; IPR002942; S4.
InterPro; IPR001305; FRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_lb.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last amotation update)
Bicarbonate transport system AFP-binding protein.
Name=cmpC; OrderedLocusNames=tlr2002;
   Last sequence update)
Last annotation update)
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35.9%; Pred. No. 22;
rative 5; Mismatches
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Pfam; PF0579; tRNA-synt lb; 1.
PRINYS; PR01040; TRNASYNTHYTR.
TIGRAMS; TIGR00234; tyrS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
PROSITE; PS50889; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
Tyrosyl-tRNA synthetase.
OrderedLocusNames=VV20878;
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Best Local Similarity 35.5.
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P00952; 2TS1.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                STRAIN=CMCP6
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"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; APRO2057; BAR9138.1; ---
GO, GO:0005489; Fielectron transporter activity; IEA.

GO; GO:0006118; Fielectron transport; IEA.

InterPro; IPR002109; Glutaredoxin.

InterPro; IPR002109; Glutaredoxin.

Pfam; PF00462; Glutaredoxin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 27.6%; Score 56; DB 2; Length 658; Local Similarity 41.4%; Pred. No. 37; and 12; Conservative 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00152; ATPASE ALPHA BETA; UNKNOWN 1.
SEQUENCE 428 AA; 48178 MW; TAEA2E3141DCAGE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 WLQMEEEEEGFEDFDPEIISSFRKSLQELPSDHPFHISNH 226
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OMAR-2004 (TrEMBLrel. 26, Last annotation update)
Emb[CAB72177.1.
Arabidopsis thaliana (Mouse-ear cress)
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0015706; P:nitrate transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003439; ABA_ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR00389; NBC_Transporter.
Probom; PD000006; ABC_transporter; I.
Probom; PD000006; ABC_transporter; I.
Probom; SM0382; AAA; I.
TIGRRAMS; TIGR01184; ntrCD; I.
PROSITE; PS00211; ABC_TRANSPORTER; I; PROSITE; PS00211; ABC_TRANSPORTER_2; I.
ATP-binding; Complete protecome.
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accumulation.
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AC22 TENMO
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                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Mimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamoti H., Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijshita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Rasawa W., Katagairi S., Kikuta A., Kobayashi M., Koni, K., Machara T., Mizuno H., Mizubayashi T., Mixai Y., Machara K., Machara T., Mizuno H., Mizubayashi T., Mixai Y., Machara T., Mizuno H., Mizubayashi T., Makamura M., Namiki M., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M., Maki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Bun M.Y., Yano M., Jiang J., Gojobori T.;
Mature 420:312-316(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae, Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
04048009.22 protein (P06988A10.19 protein).
Name=P0648009.22; Symonyms=P0698A10.19;
Oryza sativa (japonica cultivar-group).
Oryza, viridiplantae, Streptophyra, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae; Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Submitted (WAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                          Sasaki T'., Matsumoto T., Yamamoto K.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 AA; 64866 MW; 15D366ECBE93F5D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1998 (TYEMBLrel. 08, Last sequence update)
01-NOV-1998 (TYEMBLrel. 28, Last annotation update)
Hypothetical protein T01E8.5.
Name="PO1E8.5;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.3%; Score 55.5; DB 2;
43.8%; Pred. No. 37;
tive 4; Mismatches 9;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z48583; CAA88749.1; JOINED
Z48809; CAA88749.1; -.
Z48583; CAA88473.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP003922; BAB86233.1; -. EMBL; AP003297; BAB92449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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STRAIN=Bristol N2;
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SEQUENCE FROM N.A.
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                                                                                                                                                NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gramene; Q8RYX8;
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                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92097825; PubMed=1728581; Bouhin H., Charles J.-P., Quennedey B., Delachambre J.; Charles J.-P., Quennedey B., Delachambre J.; Charles J.-P., Quennedey B., Delachambre J.; Developmental profiles of epidermal mRNAs during the pupal-adult molt of Tenebric molitor and isolation of a cDNA clone encoding an adult cuticular protein: effects of a juvenile hormone analogue."; Dev. Biol. 149:112-122(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97245547; PubMed=9087546;
Bouhin H., Braquart C., Charles J.-P., Quennedey B., Delachambre J.;
"Mucleoride sequence of an adult-specific cuticular protein gene from the beetle Tenebrio molitor: effects of 20-hydroxyecdysone on mRNA
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Adult-specific cuticular protein ACP-22.
Poly-Gly.
Poly-Gly.
Poly-Gly.
S-y (in Ref. 2).
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Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Tenebrionidae, Tenebrio.
                                                                                                                                                         Length 1270;
EMBL; Z48809; CAA88473.1; JOINED.
PIR, T22615; T22615,
Wormbep; T01E8.5; CE18165.
Hypothetical protein.
SEQUENCE 1270 AA; 147634 MW; DCB661227D75F541 CRC64;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adult-specific cuticular protein ACP-22 precursor. Name=ACP22;
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                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                      :||||::|| :|| :|| 656 | 15WIEVEREMONIDARVKRIKIKDCELYEDH 656
                                                                                                                                                                                                                                                                                                                                                                                                                                          199 AA
                                                                                                                                                                                                                                                             2 LSWIEMDTEMEMLLARFRRT---PGDLHLDH 29
                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                       Score 55.5;
Pred. No. 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tenebrio molitor (Yellow mealworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X66455; CA442985.1; -. EMBL; X72783; CA451290.1; -. PIR; S16063; S16063. PIR; S32224; S32224.
                                                                                                                                                         Query Match
Best Local Similarity 41.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199
26
37
72
104
138
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387
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Pfam; PF02542; YgbB; 1
                                                                                                                           Zymomonas mobilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frameshifts.
                                                                                                                                                                                      NCBI_TaxID=542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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GO; GC:0003700; F:transcription factor activity; IEA.
GO; GC:0000156; F:two-component response regulator activity; IEA.
GO; GC:0000160; F:sensory perception; IEA.
GO; GC:0000160; P:sensory perception; IEA.
GO; GC:0000160; P:wo-component signal transduction system (p. . .; IEA.
InterPro; IPR010092; HTH_LuxR.
InterPro; IPR001092; HTH_LuxR.
FFam; PF00196; GerE; I.
Pfam; PF00196; GerE; I.
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Protecobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Rojas C.M., Ham J.H., Kim J.F., Beer S.V., Collmer A.;
Submitted (CCT-2002) to the EMBL/GenBank/DDBJ databases.
-1. SIMILARITY: Contains 1 HTH luxR-type DNA-binding domain.
EMBL, AF448202; AAM46692.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.8%; Score 54.5; DB 2; Length 213; ilarity 40.6%; Pred. No. 17; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEGUENCE FROM N.A. Hand. J.R., Rodriguez-Palenzuela P., Rojas C.M., Hamd.H., Alfano J.R., Collmer A.; Collmer A.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                       Length 199;
                                                                                 4; Indels
20710 MW; 1EBF2D1DBEC6739F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation.
SEQUENCE 213 AA; 23772 MW; 728465D54BEB4249 CRC64;
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ProDom; PD000307; HTH LUNK; 1.
ProDom; PD000039; Response_reg; 1.
SMART; SM00421; HTH LUNK; 1.
SMART; SM00448; REC; 1.
PROSITE; PS001622; HTH LUNR FAMILY; 1.
PROSITE; PS50110; RESPONSE REGILATORY; 1.
DNA-binding; Phosphorylation; Sensory transduction;
                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                     27.1%; Score 55; DB 1; 52.9%; Pred. No. 13; ative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ALGYITKDKDPEALLSAIRRVAQGARYIDHSI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEREZYMO STANDARD; PRT; 387 AA. (98RZ]; Q9SLD5; Q9SLD6; L6-OCT-2001 (Rel. 40, Created) (6-OCT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                        213 AA.
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                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                               || |:| : ::|| |||
118 TPVDVHHEEAIHLKAHP 134
                                                                                                                         21 TPGDLHLDHSVHLCAHP 37
                                                                                 Conservative
                                                                                                                                                                                                                                                                      PRELIMINARY;
199 AA;
                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserv
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SEQUENCE
                                       Query Match
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ID ISDF_ZY
AC Q9RNZI
DT 16-OCT-
DT 16-OCT-
DT 05-JUL
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Q8KUM3
                                                                                 Matches
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Query Match 26.8%; Score 54.5; DB 1; Length 387; Best Local Similarity 30.3%; Pred. No. 34; Matches 10; Conservative 13; Mismatches 9; Indels 1
CONFLICT 36 36 N -> I (in Ref. 2).
CONFLICT 63 63 T -> A (in Ref. 2).
SEQUENCE 387 AA; 41946 MW; A995805BFD952B27 CRC64;
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1; Gaps

Search completed: November 10, 2004, 13:38:33 Job time : 47.1796 secs දු පු

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7410, Ap 12, Appl 12, Appl

5, Appli 5, Appli 42251, A 17, Appl 15, Appl

1832, Ap 27294, A 321, App

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US-09-270-767-45056

) Sequence 45056, Application US/09270767

) Sequence 45056, Application US/09270767

) Patent No. 6703491.

) GENERAL INFORMATION:

) APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

PILE REFERENCE: File Reference: 7326-094

CURRENT APPLICANTON NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 45056

LENGTH: 265
                                                                                                                                                                                                                                                                                                                    Sequence 3,
                                                                                                                                                                                                                                                               Sequence 3
Sequence 4
Sequence 3
                                     Sequence Seq
                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 4; Length 54;
Pred. No. 7.6;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5801, Application US/09621976

Patent No. 6639063

GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT PILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

FEMBLE OF SEQ ID NOS: 19335

SEQ ID NO 5801
US-09-252-991A-31560

US-08-134-121-5

US-08-135-89-5

US-08-270-767-42251

US-08-867-0878-17

US-08-867-0878-17

US-08-867-12

US-09-543-681A-7410

US-09-543-681A-7410

US-09-98-12

US-09-98-12

US-09-98-12

US-09-139-637A-321

US-09-125-991A-27294

US-09-125-991A-27294

US-09-252-991A-27294

US-09-252-991A-24404

US-09-252-991A-24404

US-09-252-991A-24404

US-09-252-991A-24404

US-09-252-991A-24404

US-09-252-991A-2404

US-09-134-001C-3991

US-09-134-01C-3991

US-08-144-11-3

US-08-134-01-3
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ORGANIEM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
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     ; LOCATION: -46..-1
US-09-621-976-5801
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NAME/KEY: SIGNAL
LOCATION: -46..-1
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Sequence 2, Appli
Sequence 2, Appli
Sequence 255, App
Sequence 21166, A
Sequence 40047, A
Sequence 40047, A
Sequence 52263, A
Sequence 12958, A
Sequence 12958, A
Sequence 11540, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
                                                                                                                                  November 10, 2004, 12:32:37; Search time 3.79965 Seconds (without alignments) 191.991 Million cell updates/sec
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Sequence 5
Sequence 4
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(c) 1993 - 2004 Compugen Ltd.
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US-09-770-774-5056

US-09-510-011A-5

US-09-583-110-4701

US-08-8819-458A-16

US-09-393-627B-3

US-09-393-627B-3

US-09-393-627B-3

US-09-758-008-2

US-09-758-008-2

US-09-758-008-2

US-09-758-008-2

US-09-758-008-2

US-09-468-039-2

US-09-225-391A-21166

US-09-227-4074

US-09-227-991A-21166

US-09-227-991A-21166

US-09-227-991A-21166

US-09-227-991A-21166

US-09-227-991A-21166

US-09-227-991A-21166

US-09-270-76-4047

US-09-489-039A-11540

US-09-489-039A-11540

US-09-488-039A-11540

US-09-488-038A-11540

US-09-488-038A-11540

US-09-388-546-18

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US-09-659-084-18
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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57
1 TSTLPHIRRTR 11
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                                               Copyright
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Match
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Perfect score:
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                                                                                                      OM protein -
                                                                                                                                                                                                                                                       Sequence:
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No.
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Gaps

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US-09-270-767-45056

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WS-09-252-991A-22955

Sequence 22955, Application US/09252991A

TITLE OF INVENTION: AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ASSURED ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ASSURED ACID AND AMINOSES: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                     APPLICANT: Jensen, Ejner B.
APPLICANT: Cherry, Joel
APPLICANT: Cherry, Joel
APPLICANT: Blrod, Susan L.
ITILE OF INVENTION: Methods For Producing Polypeptides
TITLE OF INVENTION: In Respiratory-Deficient Cells
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,458A
FILING DATE: 17-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5215.000-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                                                                   Sequence 16, Application US/08819458A Patent No. 5891669 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 72.7
Matches 8; Conservative
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US-08-819-458A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 10174
                                     US-08-819-458A-16
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APPLICANT: LYDORNATION:
APPLICANT: LYDORNATION:
APPLICANT: LYDORNATION:
APPLICANT: LYDORNATION: Pucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: Pucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: Pucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: PROPORTY (1500-05-26 PRIOR APPLICATION NUMBER: US/09/583,110 CURRENT FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/107,433 PRIOR FILING DATE: 1998-06-30 PRIOR PLING DATE: 1998-06-30 PRIOR PLING DATE: 1998-06-30 PRIOR FILING DATE: 1998-06-30 PRIOR FILING DATE: 1997-07-02 PRIOR FILING DATE: 1997-07-07 PRIOR FILING DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ratliff, Timothy
APPLICANT: Ratliff, Timothy
TILE OF INVENTION: METHOD FOR INHIBITING INFLAMMATORY RESPONSES
TILE OF INVENTION: WETHOD FOR INHIBITING INFLAMMATORY RESPONSES
FILE REFERENCE: 140.0010 0.01
CURRENT APPLICATION NUMBER: US 60/121,177
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 381
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0
                                     Score 36; DB 4; Length 265; Pred. No. 43; 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.2%; Score 36; DB 4; Length 420; Best Local Similarity 75.0%; Pred. No. 71; Matches 6; Conservative 1; Mismatches 1; Indels
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Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09510031A
Patent No. 6638518
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                              63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT

ORGANISM: Mycobacterium avium
US-09-510-031A-5
Query Match
Best Local Similarity 66...
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124 TQALPHLRR 132
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TYPE: PRT

CRGANISM: Adenovirus
US-09-758-008-4
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STATE: CA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304
                                                                                                                                                                                                                                                                                    LENGTH: 362
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                                      61.4%; Score 35; DB 4; Length 325; 63.6%; Pred. No. 82; ive 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35, DB 4; Length 362;
Pred. No. 92;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                               Facence No. 645314

Facence No. 645314

GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Rocead, Imre
APPLICANT: Roclvink, Petrus W.
APPLICANT: Bruder, Joseph T.
TITLE OF INVENTION: Alternatively Targeted Adenovirus
FILE REFERENCE: 202345
CURRENT PILIOR DATE: 1999-09-10
FRIOR FILING DATE: 1999-09-10
FRIOR APPLICATION NUMBER: US 60/099,851
FRIOR PILING DATE: 1999-09-10
FRIOR FILING DATE: 1999-05-28
FRIOR FILING DATE: 1999-05-28
FRIOR FILING NAME: 1999-05-28
SOFTWARE: Patentin Ver. 2.2
SEQ ID NO. 3
LENGTH 362
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US-09-758-008-2
Sequence 2, Application US/09758008
Sequence 2, Application US/09758008
Sequence 10. Application US/09758008
TITLE OF INVENTION:
TITLE OF INVENTION: Adenovirus serotype 30 (Ad30)
FILE REFRENCE: 875.044USI
CURRENT APPLICATION NUMBER: US/09/758,008
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Human adenovirus serotype 9
US-09-393-627B-3
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70.0%;
                     Query Match
Best Local Similarity 63.6
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Best Local Similarity 70.0
Matches 7; Conservative
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273 SSTLPALRRRR 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Adenovirus
US-09-758-008-2
US-09-252-991A-22955
                                                                                                                                                                                                                          RESULT 7
US-09-393-627B-3
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PRESULT, 9

DESCRIPT, 9

DESCRIPT, 9

DESCRIPT, 9

DESCRIPT, 100, 663546

DESCRIPT, 100, 663546

DESCRIPT, 100, 663546

TITLE OF INVESTION; Administration, Ad
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0
                                                                                         61.4%; Score 35; DB 2; Length 638; 70.0%; Pred. No. 1.7e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 884;
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                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08465976A
Petent No. 5669632
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: LI, YI
APPLICANT: RUBEN, CRAIG A
TITLE OF INVENTION: HUWAN G-PROTEIN RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE CARELLA, BYRNE, BAIN GILFILLAN, CECCHI
ADDRESSEE: STEWART & OLSTEIN
CITY: ROSELAND
CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: ...
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,976A
FILING DATE: 06-UN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PERRAPO GREGORY IN
REGISTRATION NUMBER: 36,134
RECISTRATION NUMBER: 36,134
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08982412
Patent No. 5958729
GENERAL INFORMATION:
APPLICANT: SOFPET, DANIEL R
APPLICANT: LI, YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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illarity 80.0%;
Conservative
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amino acid
                                                                                           Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                       1 TSTLPHIRRT 10
                                                                                                                                                                                              84 TGTLPRIHRT 93
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Best Local Similarity
Matches 8; Conserva
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 205011
US-08-681-151-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                JS-08-465-976A-2
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US-08-982-412-2
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APPLICANT: ROSSA, CRAIG A MANABELLOAN: ROSSA, CRAIG A MANABELOAN: ROSSA, ROSSA
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Gaps

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59.6%; Score 34; DB 4; Length 159; 63.6%; Pred. No. 58; ive 2; Mismatches 2; Indels
                            TELEPHONE: (781) 893-8277
TELEPACK: (781) 893-8277
INFORMATION FOR SEQ ID NO: 4074:
SEQUENCE CHRRACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...159
SEQUENCE DESCRIPTION: SEQ ID NO: 4074:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: November 10, 2004, 13:44:06 Job time: 4.79965 secs
              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    US-09-107-532A-4074
                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                           Sequence 21166, Application US/09252991A
Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ABEUGATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21166
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4074, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
                                                    Gaps
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Query Match 59.6%; Score 34; DB 4; Length 144; Best Local Similarity 70.0%; Pred. No. 52; Matches 7; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.6%; Score 34; DB 4; Length 146; Best Local Similarity 77.8%; Pred. No. 53; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7un-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/01571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21166
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                                                                                            1 TSTLPHIRRT 10
                                                                                                                                    26 TSLNPHIRNT 35
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US-09-252-991A-21166
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US-09-107-532A-4074
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Sequence 170498, Sequence 25867, Sequence 10591, Ap Sequence 152417, Sequence 152417, Sequence 152417, Sequence 1544, Ap Sequence 3144, Ap Sequence 3444, Ap Sequence 25414, Sequence 25414, Sequence 254, App Sequence 354, App Seq
                                                                                                                                                                                                                                                                             3324, App
3554, App
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 354, Sequence 354, Sequence 354, Sequence 354, Sequence 354, Sequence 354,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/10092750
| Sequence 34, Application US/10092750
| Publication No. US20030032157A1
| GENERAL INFORMATION:
| APPLICANT: Hammond, Philip W.
| APPLICANT: Alpin, Julia
| APPLICANT: Wright, Martin C.
| TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
| FILE REFERENCE: 50036/050002
| CURRENT APPLICATION NUMBER: US/10/092,750
| CURRENT FILING DATE: 2002-03-07
| PRIOR FILING DATE: 2001-03-08
| NUMBER OF SEQ ID NOS: 253
| SEQ ID NOS: 253
| SEQ ID NOS: 253
| SEQ ID NOS: 253
                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 242274, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
 TSTLPHIRRTR 11
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ORGANISM: Homo sapiens
US-10-092-750-34
US-10-424-599-242274
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US-10-092-750-34
 RESULT 2
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Sequence 8110, Ap
Sequence 25181,
Sequence 7411, A
Sequence 46417, A
Sequence 4217, A
Sequence 22379, Ap
Sequence 22379, Ap
Sequence 6100, Ap
Sequence 6100, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Appl
Sequence 242274,
Sequence 202505,
                                                                                                         November 10, 2004, 16:36:12 ; Search time 11.8169 Seconds (without alignments) 328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1: \cgn2 \( \) \cgn2 \( \
                                                                                                                                                                                                                                                                                                                              1566620
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-092-750-34
US-10-424-599-242274
US-10-437-963-26255
US-10-156-761-8110
US-10-424-599-255181
US-10-424-599-255181
US-10-767-701-46417
US-10-767-701-46417
US-10-369-493-42379
US-10-369-498-7454
US-10-369-4988-76100
US-10-437-963-189053
                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                           1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                         US-10-092-750-34
57
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Match Length DB
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28
339
339
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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12646046014121

Result

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Sequence 252181, Application US/10424599

Sequence 252181, Abplication US/2040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57404, Application US/10425114
Sequence 57404, Application US/10425114
Sublication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Roomyei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 67;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: PAT_MRT3847_69748C.1.pep
US-10-424-599-252181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FLIENG DATE: 2001-05-30
PRIOR FLIENG DATE: 2001-05-30
FRIOR FLIENG DATE: 2001-05-30
FRIOR FLIENG DATE: 2001-05-30
FRIOR FILING DATE: 2001-08-02
FRIOR FILING DATE: 2001-08-02
FRIOR FILING DATE: 2001-08-02
FRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Streptomyces avermitilis
US-10-156-761-8110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 70...
Fest Local 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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275 STTPHLRRAR 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-252181
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: W. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbauuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
UNUMBER OF SEQ ID NOS: 204966
SEQ ID NO 202505
       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF EQ ID NOS: 285684
SEQ ID NO 242274
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

86.0%; Score 49; DB 15; Length 28;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels
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US-10-424-599-242274
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US-10-437-963-202505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 202505, Application US/10437963; Publication No. US20040123343A1
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Best Local Similarity 72.7
Matches 8; Conservative
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442 TSTVPNIERTR 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-437-963-202505
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APPLICANT:
APPLICANT:
APPLICANT:
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us-10-092-750-34.rapb

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Sequence 4205, Application US/10369493

Sequence 4205, Application US/10369493

Publication No. US2030333675A1

GENERAL INFORMATION:
APPLICANT: Cano, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILE REPERSENCE: 38-10($205.)B
CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 4205

LENGTH: 903
PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR PLLING DATE: 2000-05-26

PRIOR PLLING DATE: 2000-05-26

PRIOR PLLING DATE: 2000-05-26

PRIOR PLLING DATE: 2000-09-09

PRIOR PLLING DATE: 2000-09-09

PRIOR PLLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-23

PRIOR PLLING DATE: 2000-10-22

PRIOR PLLING DATE: 2000-11-22

PRIOR PLLING DATE: 2000-12-22

PRIOR PLLING DATE: 2000-12-22

PRIOR PLLING DATE: 2000-10-2-16

PRIOR PLLING DATE: 2000-10-22

PRIOR PLLING DATE: 2000-10-22

PRIOR PLLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-216

PRIOR PLLING DATE: 2001-02-16

PRIOR PLLING DATE: 2001-03-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 15; Length 898;
Pred. No. 4.1e+02;
1; Mismatches 1; Indels
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US-10-369-493-22379
; Sequence 22379, Application US/10369493
; Publication No. US20030233675A1
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US-10-369-493-4205
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Matches 8; Conservative
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CORGANISM: Vibrio cholerae
US-10-282-122A-77110
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287 SSTLSHLRRT 296
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Matches 7; Conserv
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US-10-767-701-46417
Sequence 46417, Application US/10767701
Sequence 46417, Application US/20040172684A1
Sequence 46417, Application No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-71 (5355)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 46417
LENGTH: 176
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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US-10-767-701-46417
                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17344G01_FLI.pep
US-10-425-114-57404
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; Sequence 77110, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
          CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 57404 LENGTH: 131
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yangmoto, Robert
APPLICANT: Yangmoto, Robert
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Matches 6; Conservative
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ORGANISM: Sorghum bicolor
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ORGANISM: Zea mays
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Gaps

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Sequence 189033, Application US/10437963
; Sequence 189033, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbaruk, Brad
APPLICANT: Brants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION INVERS: US/10/437,963
CURRENT FILNG DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 189053
LENGTH: 100
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: About Vibua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT APPLICATION NUMBER: US/10/428
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 242031
LENGTH: 116
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Pred. No. 66;
1; Mismatches 2; Indels
                                                                                                                                                               64.9%; Score 37; DB 11; Length 70; 75.0%; Pred. No. 46; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_85599C.1.pep
US-10-437-963-189053
SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 6100 LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 242031, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.9%;
                                                                                                                                             Query Match
Best Local Similarity 70.0
Trans 7; Conservative
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                                                                                         , ORGANISM: Homo sapiens
US-09-864-408A-6100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                              30 STLPHLRK 37
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                             2 STLPHIRR 9
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NAME/KEY: unsure
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US-10-424-599-242031
                                                                          TYPE: PRT
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Publication No. US20040009474A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INFORMATION No. US20040009474A1el Human Polynucleotides and Polypeptides Enco TITLE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 906e
              APPLICANT: Goo, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22379
LENGTH: 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7454, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bo, Jiang
APPLICANT: Howard, Buseey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3:1
SEQ ID NO 7454
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Pred. No. 5.7e+02;
2; Mismatches 1; Indels
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Pred. No. 5.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Saccharomyces cerevisiae US-10-369-493-22379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Candida albicans
US-10-032-585-7454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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489 SSTLSHLRRT 498
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484 SSTLSHLRRT 493
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    GENERAL INFORMATION:
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US-09-864-408A-6100
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US-10-032-585-7454
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LILLE OF INVENTION: ALLO MAINTED ACID MOLECULES and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21/53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-06-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 170498 LENGTH: 208
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Best Local Similarity 72.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                     Ouery Match

Best Local Similarity 87.5%; Pred. No. 77;

Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure;
COCATION: (1)..(208)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_68819C.1.pep
US-10-437-963-170498
; LOCATION: (1)..(116)
; OTHER INFORMATION: unsure at all Xaa locations FALTER INFORMATION: Clone ID: PAT_MRT3847_60581C.1.pep US-10-424-599-242031
                                                                                                                                                                                                                                                                                                                                                           Sequence 170498, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua, APPLICANT: Tow, Yihua, APPLICANT: Wu, Wei, APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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                                                                                                                                                                                                                                                   104 TLPHIRMT 111
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US-10-437-963-170498
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Search completed: November 11, 2004, 01:28:16 Job time: 12.8669 secs

15 TSTTPRPRRTR 25

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 2.45078 Seconds (without alignments) 431.857 Million cell updates/sec on:

Title: Perfect score:

US-10-092-750-34 57 1 TSTLPHIRRTR 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79: *
2: pir1: *
3: pir2: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CIMMADIES

		dР			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	DI	Description
;	40	70.2	898	2	F89500	protein T27A10.6 [
~	38	66.7	42	N	69	tical p
m	38	66.7	738	N	œ	A.
4	38	66.7	868	N	A82298	translation initia
ιO	38	66.7	1224	(7	m	DNA-directed RNA p
9	37	4	383	(7	97	conserved hypothet
7	37	4	1210	N	S35548	DNA-directed RNA p
œ	37	4	1879	67	T15962	hypothetical prote
6	36	3	64	7	C64010	-1
	36	m	107	0	T44914	hypothetical prote
11	36	63.2	314	7	T36913	۳
12	36	m	355	۳H	S22181	gamma-1-microglobu
13	36	m	422	N	C95053	
14	36	m	772	~	T30645	
15	36	63.2	808	7	JQ2205	UL47h protein - Ma
16	36	63.2	919	N	T32541	
11	36	63.2	947	H	B44294	unc-5 protein, lon
18	36	63.2	1095	N	AD0301	conserved hypothet
13	36	63.2	1134	Н	A29944	chaoptin precursor
50	35	61.4	278	N	E75546	conserved hypothet
21	35	61.4	305	C)	A38422	insulin-like prote
22	35	61.4	362	~	S37220	fiber protein - hu
23	35	61.4		N	\$40092	fiber protein - hu
24	35	61.4	366	~1	T25178	hypothetical prote
25	35	61.4	556	N	G70503	probable cycA prot
56	35	61.4	591	(7)	T02402	beta-glucosidase h
27	35	61.4	638	н	KOMSPL	plasma kallikrein
28	35	61.4	638	-	KORTPL	plasma kallikrein
50	35	61.4	1137	N	T02097	alutamate synthase

MEGF2 protein - hu	ferredoxin-depende	glutaredoxin (grx-	probable acetyltra	hypothetical prote	hypothetical prote	conserved hypothet	probable lipJ prot	hypothetical prote	amino acid regulat	hypothetical prote	hypothetical prote	translation initia	probable ATP-depen	hypothetical prote	coagulation factor
T00250	C84839	G69441	T35305	T03041	T20063	T36104	A70518	C96621	A13370	E96492	F96502	C75351	C71367	F96581	KFHU1
7	7	~	~	N	0	N	N	N	7	N	N	~	н	N	Н
1364	1629	82	169	236	318	436	462	474	486	538	570	597	607	622	625
61.4	61.4	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6
35	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	4.2	43	44	45

ALIGNMENTS

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Postein T27A10.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Saces: 10.4 May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Acces: 10.7 May-2012 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
S;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000, MUID: 99059613; PMID: 9851916
A;Note: sew websites genome wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Restudus: preliminary
A;Molecule type: DNA
A;Residues: 1-868 cSTO-A;Cross-references: UNIPROT:Q22822; GB:chr_X; PIDN:AAB52504.1; PID:g1326288; GSPDB:GN000;
C;Generics: T27A10.6
A;Map position: X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.2%; Score 40; DB 2; Length 868; 72.7%; Pred. No. 17; ive 0; Mismatches 3; Indels
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Matches 8; Conserva
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RESULT 2

PRESCRIPTION TRIBED [imported] - Xylella fastidiosa (strain 9a5c)
C'Species: Xylella fastidiosa
C'Accession: F83691
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent Nature 406, 151-157, 200
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUD:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Recession: F82691
A;Status: preliminary
A;Rocession: F82691
A;Residues: 1-42 <SIMA
A;Residues: 1-42 <SIMA
A;Residues: 1-42 <SIMA
A;Residues: UNA
A;Residues: 1-42 <SIMA
A;Residues: UNA
A;Residues: 1-42 <SIMA
A;Residues: UNA
A;Resi

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A; Gene: XF1351

d 8

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DNA-directed RNA polymerase (EC 2.7.7.6) II 140K chain [validated] - yeast (Saccharomyces NyAlternate names: DNA-directed RNA polymerase B chain B150; protein 03533; protein YORI: C;Species: Saccharomyces cerevisiae
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: A25884; S36660; A37894; S67039
R;Sweetser, D.; Nonet, M.; Young, R.A.
A;Title: Prokaryotic and eukaryotic RNA polymerases have homologous core subunits.
A;Reference number: A25884; MUID:87147239; PMID:3547406
A;Accession: A25884
                                                                                   C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homol
F;400-509/Domain: translation elongation factor Tu homology <ETU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 11224 <SWE>
A;Cross-references: UNIPROT:P08518; EMBL:M15693; NID:g172210; PIDN:AAA68096.1; PID:g17221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 961-990 <RIV>
K.Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winso:
Submitted to the Protein Sequence Database, July 1996
A;Reference number: S67032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
XResidues: 1-1224 <BOR>
A;Cross-references: EMB1:Z75059; NID:g1420378; PIDN:CAA99357.1; PID:g1420379; MIPS:YOR153
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R,Sweetser, D.; Nonet, M.; Young, R.A.
submitted to the EMBL Data Library, July 1987
A;Description: Prokaryotic and eukaryotic RNA polymerases have homologous core subunits.
A;Reference number: S36860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Description: BC 2.7.7.6 [validated, MUID:87147239]
C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Molecule type: DNA
A; Gesdidues: 1-1002, RRRY', 1007-1224 <SW2>
A; Cross-references: EMBL:M15693; NID:9172210; PIDN:AA468096.1; PID:9172211
R;Riva, M.; Carles, C.; Sentenac, A.; Grachev, M.A.; Mustaev, A.A.; Zaychikov, E.F.
J. Biol. Chem. 265, 16498-16503, 1990
A; Title: Mapping the active site of yeast RNA polymerase B (II).
A;Reference number: A37894; MUID:90375520; PMID:2204624
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                        Length 898;
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Pred. No. 58;
2, Mismatches
                                                                                                                                                                                        Score 38; DB 2
Pred. No. 42;
1; Mismatches
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                                                                                                                                                                                        66.7%;
ilarity 80.0%;
Conservative
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ilarity 70.0%;
Conservative
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413 TSTLDYIRRT 422
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Matches 8; Conserv
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Best Local Similarity
Matches 7; Conserv
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J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiguchado, M.A.; Madeira, A.M.B.N.; Madeira, H.N.F.; Marino, C.L.; Marques, M.V.; Martins, B.A.; Aluthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.Atuthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva and Jr.; W.A.; da Silva; M.A.; Verfovski-Almeida, G.; Vettore, A.L.; Z., Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. J. R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MJID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: S01892
R;Alm, R.A.; Strocher, U.H.; Manning, P.A.
R;Alm, R.A.; Strocher, U.H.; Manning, P.A.
A)C1. Microbiol. 2, 481-488, 1988
A;Title: Extracellular proteins of Vibrio cholerae: nucleotide sequence of the structura in the non-haemolytic classical strain 569B.
A;Reference number: S01892; MUID:89013889; PMID:3050359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Cross-references: UNIPROT:Q9KU80; GB:AE004150; GB:AE003852; NID:g9655075; PIDN:AAF938d; Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation initiation factor IF-2 VC0643 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Alterander names: El Tor hemolysin
C;Species: Vibrio cholerae
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 10-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Superfamily: Vibrio hemolysin A
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-738/Product: hemolysin A #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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Pred. No. 1.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 2
Pred. No. 34;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: Y00557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|| |||
STMPHQHRTR 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STLPHIRRTR 11
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TNTLPHVR 166
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A; Molecule type: DNA A; Residues: 1-738 < ALM>

A; Accession: S01892

1 TSTLPHIR

ઠ g

159

A, Residues: 1-898 <HEI>

A; Map position: 1

Genetics:

A, Status: preliminary A, Molecule type: DNA

A; Accession: A82298

us-10-092-750-34.rpr

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A,Molecule type: DNA
A,Residues: 1-1879 <FAV>
A;Cross-references: UNIPRCT:Q19161; EMBL:U46672; NID:g1166599; PID:g1166600; PIDN:AAA857:
C;Genetics:
A;Gene: CESP:P07C7.1
A;Introns: 818/1; 1522/1; 1702/3; 1784/1
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A;Molecule type: DNA
A;Residues: 1-64 <TIGR>
A;Cross-references: UNIPROT:P44021; GB:U32741; GB:L42023; NID:g1573582; PIDN:AAC22259.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C64010

hypothetical protein HI0592 - Haemophilus influenzae (strain Rd KW20)

Cispecies: Haemophilus influenzae

Cispecies: Haemophilus influenzae

Cispecies: Haemophilus influenzae

Cipacession: C64010

Cipacession: C64010

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Fifeischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Fifeischmann, R.D.; Fritchman, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: C64010

A;Accession: C64010
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C;Accession: T44914
R;Parkhill, J; Barrell, B.G; Rajandream, M.A.
Sibmitted to the EMBL Data Library, August 1997
A;Reference number: Z22864
A;Accession: T44914
A;Reference number: Z22864
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-107 <-PAR-A;Residues: 1-107 <-PAR-A;Residues: 1-107 <-PAR-A;Residues: UNIPROT:032980; EMBL:Z98741; PIDN:CAB11414.1
C;Genetics:
C;Genetics:
A;Note: MLCB22.49
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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54 TSSMPEVRRRR 64
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SLMAHIRRTR 37
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Best Local Similarity
Matches 6; Conserva
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T36913
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S35548

DNA-directed RNA polymerase (EC 2.7.7.6) II chain 2 - fission yeast (Schizosaccharomyces C.Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 355548
C;Cosceric acid sequence not shown
C;Accession: 35554
C;Accession: 3554
C;Accession: 35554
C;Acces
C;Accession: D89975

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguda, M.; Mizutani Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

Lancet 357, 1225-1240, 2001

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUD:21311952; PMID:11418146

A;Recession: D89975

A;Recus: preliminary

A;Residues: 1-383 < KUR>
A;Residues: 1-383 < KUR>
A;Coss-references: UNIPROT:Q99704; GB:BA000018; PID:g13701670; PIDN:BAB42963.1; GSPDB:GGGenetics:
A;Genetics:
A;Genetics:
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T15962
T15962
C)Posterical protein F07C7.1 - Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C)Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C)Accession: T15962
R)Favello, T.
R)Favello,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 89;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 383
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Pred. No. 27;
2; Mismatches
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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195 STLPHLRK 202
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A, Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host res
A, Reference number: Z20876; MUID:96325459; PMID:8670425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Marek's disease virus homologue
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A;Residues: 1-808 «YAN»
A;Cross-references: UNIRNOT:Q69320; GB:L10283; NID:G388703; PIDN:AAA03150.1; PID:G388708
A;Experimental source: strain GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T30645
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss,
Science 273, 813-816, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Marek's disease virus
Cispecies: Marek's disease virus
Cipaceston: UQ2205
Riyanagida, N.; Yoshida, S.; Nazerian, K.; Lee, L.F.
J. Gen. Virol. 74, 1837-1845, 1993
A;Title: Nucleotide and predicted amino acid sequences of Marek's disease vi
A;Reference number: UQ2199; MUID:93389438; PMID:8397281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Note: MC043L
C;Superfamily: Molluscum contagiosum virus 1 hypothetical protein 43L
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                                                                                                                                                   Query Match 63.2%; Score 36; DB 2; Length 422; Best Local Similarity 75.0%; Pred. No. 46; Astches 6; Conservative 1; Mismatches 1; Indels
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Best Local Similarity 70.0%; Pred. No. 86,
Matches 7; Conservative 0; Mismatches 3; Indels
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                                           A,Gene: SP0460
C,Superfamily: Lactobacillus delbrueckii ISL3 transposase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 43L - Molluscum contagiosum virus 1 N/Alternate names: MCO43L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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UL47h protein - Marek's disease virus
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    C; Genetics
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Adeces: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Adecesion: C95653
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-314 <SEE>
A;Residues: 1-314 <SEE>
A;Cross-references: UNIPROT: Q9X9X3; EMBL: AL096743; PIDN: CAB46400.1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3(2)
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A, Molecule type: DNA
A, Fasiduse: 1.422 - KURA
A, Fasiduse: 1.422 - KURA
A, Cross-references: UNIPROT: 097SC5, GB: AE005672, PIDN: AAK74620.1, PID: g14971930, GSPDB:G
A, Experimental source: strain TIGR4
                                                                                                                     C;Accession: T36913
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
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probable integral membrane sugar transport protein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Pleuronectes platessa (plaice)
C;Accession: S22181
R;Leaver, M.J
submitted to the EMBL Data Library, December 1991
A;Reference number: S22181
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85.7%; Pred. No. 34;
tive 1; Mismatches 0; Indels
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54.5%; Pred. No. 38;
ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: inner membrane protein ugpA
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Best Local Similarity 85.
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A;Accession: T36913
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TLPHLRR 231
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A;Molecule type: mRNA
A;Residues: 1-355 <LEA>
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RESULT 12

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Best Loc Matches

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us-10-092-750-34.rup

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

November 10, 2004, 12:27:34 ; Search time 13.4318 Seconds

(without alignments)

471.205 Million cell updates/sec
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(without alignments)
Title: US-10-092-750-34
Perfect score: 57
Sequence: 1 TSTLPHIRRTR 11

Searched: 1825181 segs, 575374646 residues

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters: 182518

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt_02:* 1: uniprot_sprot:* 2: uniprot_trembl:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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% Query Match Length	75.4	73.7	73.7	73.7	71.9	71.9	ö	70.2	68.4	67.5	66.7	66.7	66.7	66.7	ė.	66.7	66.7	66.7	66.7	66.7	66.7	66.7	ġ.	66.7	66.7	66.7	66.7	66.7	
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Q6jeg8 clavispora Q6jeh9 candida nor Q6jeh2 saccharomyc Aal12527 candida n Aal12538 clavispor Q6jeh7 saccharomyc Q6jeh1 candida gla Aal12525 saccharom Q6dn95 lodderomyce Q6jeh0 kluyveromyc Q6jeh0 kluyveromyc Q6jeh0 kluyveromyc
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ALIGNMENTS

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"Structure-inctional organization of exopolysaccharide biosynthetic genes in Rhizobium leguminosarum bv. viciae VF39."; Mol. Biol. (Mosk.) 32:797-804(1998).
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01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CA2749|IPF11465 Candida albicans IPF11465 unknown
function.
                                                                                                                                                                                                                             STRAIN=VF39;
MEDLINE=99113394; PubMed=9914965;
Sadykov M.R., Ivashina T.V., Kanapin A.A., Shliapnikov M.G.,
Ksenzenko V.N.;
                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Rhizobium leguminosarum (blovar viciae).
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobiane.
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InterPro; IPR001440; TPR.
InterPro; IPR008941; TPR-like.
PROSITE; PS50293; TPR_REGION; 1.
Hypothetical protein.
SEQUENCE 615 AA; 68091 MW; EF24ABAB2CIDB04E CRC64;
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                                  615 AA.
                                  PRT;
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Best Local Similarity 88.9
Matches 8; Conservative
                                PRELIMINARY;
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=387;
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VF39;
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Q6CG25
ID Q6CG;
AC Q6CG;
DT 01-0
DT 01-0
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RESULT 1
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Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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505 TSTLSHLRRT 514
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SEQUENCE FROM N.A.
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SEQUENCE
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Matches
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Q6Z4N7
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Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
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Pubmed=15070748).
Liu V.J., Hall B.D.,
"Body plan evolution of ascomycetes, as inferred from an RNA
"Body plan evolution of ascomycetes, proc. Natl. Acad. Sci. U.S.A. 101:4507-4512 (2004).
Proc. Natl. Acad. Sci. U.S.A. 101:4507-4512 (2004).
ORFNames=YALIOBO14529;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382128; CAG82604.1; -
SEQUENCE 465 AA; 52869 WW; 1D56E4BE4CBBBC88 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DNA-dependent RNA polymerase II second largest subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1114 AA.
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InterPro; IPR007121; RNA pol B.
InterPro; IPR007644; RNA pol Rpb2 1.
InterPro; IPR007642; RNA pol Rpb2 2.
InterPro; IPR007645; RNA pol Rpb2 3.
InterPro; IPR007645; RNA pol Rpb2 4.
InterPro; IPR007646; RNA pol Rpb2 4.
InterPro; IPR007646; RNA pol Rpb2 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wincker P., Souciet J.L.; "Genome evolution in yeasts."; Nature 430:35-44(2004).
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Best Local Similarity 63.6
Matches 7; Conservative
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| 174 TSSIPHVRFTR 184
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                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                           NCBI TaxID=4952;
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QGRYHB;
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Cryptococcus neoformans (Filobasidiella neoformans).
Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
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80.0%; Pred. No. 46;
ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                            73.7%; Score 42; DB 2; Length 1114; 80.0%; Pred. No. 46; 1; Indels tive 1; Mismatches 1; Indels
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"Body plan evolution of ascomycetes, as inferred from an polymerase II phylogeny.";
Proc. Natl. Acad. Sci. U.S.A. 101:4507-4512(2004).
EMBL; AY485619; AAS67509.1; -.
Pfam; PP04563; RNA_pol_Rpb2_1; 1.
Pfam; PP04561, RNA_pol_Rpb2_2; 1.
Pfam; PP04566; RNA_pol_Rpb2_3; 1.
Pfam; PP04566; RNA_pol_Rpb2_4; 1.
Pfam; PP04566; RNA_pol_Rpb2_4; 1.
Pfam; PP04566; RNA_pol_Rpb2_6; 1.
Pfam; PP05662; RNA_pol_Rpb2_6; 1.
PROSITE; PS01166; RNA_Pol_Refax; 1.
DNA_directed RNA_polymerase; Transcription; Transferase.
NON TER 1114 1114
SEQÜENCE 1114 AA; 125436 MW; C74396ABDF649CBF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1114 AA; 125436 MW; C74396ABDF649CBF CRC64;
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14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DNA-dependent RNA polymerase II second largest subunit
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative r40c1 protein.
Name=05JNBa0060017.9;
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nes 8; Conservative
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Best Loc Matches

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"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:226-531 (2003).

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005544; F:ATP binding; IEA.

InterPro; IPR001594; ATPhind ArPase.

InterPro; IPR001932; PP2C-like.
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01-NRA-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-OCT-2003 (TrEMBLrel. 25, Last annotation update)
03-OCT-2003 (TrEMBLRel. 25, Last an
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                   Pfam; PF02518; HATPase c; 1.
SWART; SW00387; HATPase c; 1.
SWART; SW00331; PP2C_SIG; 1.
Complete protecome; Hypothetical protein.
SEQUENCE 339 AA; 36011 MW; 0D3A5258234F898F CRC64;
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PIR; F89500; R89500.
Wormbep; T27Al0.6; CE30193.
Hypotherical protein.
SEQUENCE 870 AA; 98207 WW; B3AC8105E0308A45 CRC64;
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
        Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Matches 7; Conser
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Q22822;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae, Oryzeae, Oryza, Oryza sativa.
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MEDLINE=21477403; PubMed=11572948;
MEDLINE=21477403; PubMed=11572948;
MEDLINE=2.1477403; PubMed=11572948;
MEDLINE=2.1477403; PubMed=11572948;
MENCH S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces avermitilis.
Bacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=31903,
                                                  71.9%; Score 41; DB 2; Length 402; 63.6%; Pred. No. 23; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2; Length 402;
Pred. No. 23;
2; Mismatches 2; Indels
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP005167; BAG3803.1;
SEQUENCE 402 AA; 44455 MW; 667C4859F72E7589 CRC64;
402 AA; 44455 MW; 667C4B59F72E7589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                             402 AA
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MEDLINE=22608306; Pubmed=12692562;
                                                                                                                                                                                                                                                                                                                                                              BAC83803;
02-MAR-2004 (TrEMBLrel. 27, C:
02-MAR-2004 (TrEMBLrel. 27, L:
02-MAR-2004 (TrEMBLrel. 27, L:
Putative r40c1 protein.
0SJNBA0660017,9.
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01-JUN-2003 (TrEMBLrel. 24, C:
01-JUN-2003 (TrEMBLrel. 24, L:
01-MAR-2004 (TrEMBLrel. 26, L:
Hypothetical protein.
OrderedLocusNames=SAV568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.9%;
                                                                           Local Similarity 63.6
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200 TATTPHLRSTR 210
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                                                                                                                                                        1 TSTLPHIRRTR 11
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Best Local Similarity
Matches 7; Conserva
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RESULT 7
0820E1
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Phosphorylation, Receptor, Sensory transduction.
SEQUENCE 762 AA, 85320 MW, F9071592179EA3CE CRC64;
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Q9PDM8
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Q9XJ17
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GO; GO: 0016620; C: membrane; IEA.
GO; GO: 0003677; F: ATP binding; IEA.
GO; GO: 0003677; F: DNA binding; IEA.
GO; GO: 0004872; F: receptor activity; IEA.
GO; GO: 0000156; F: two-component response regulator activity; IEA.
GO; GO: 0000156; F: two-component sensor molecule activity; IEA.
GO; GO: 0000156; F: two-component signal transduction system (p. . .; IEA.
INTERPRO; IPR001006; Chev_like.
InterPro; IPR011006; Chev_like.
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Xie C., Zhang Z.G., Zhang J.S., He X.J., Cao W.H., He S.J., Chen S.Y.;
"Spatial expression and characterization of a putative ethylene
receptor protein NTHK1 in tobacco.";
Plant Cell Physiol. 43:810-815(2002).
                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eddicotyledons, core eudicots; asterids, lamids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                      EXQUENCE FROM N.A.

Zhang J.-S., Xie C., Liu F., Liu F., Chen S.-Y.;

"A novel tobacco gene coding for a product similar to bacterial two-component regulators.";

Chin. Sci. Bull. 44:1025-1029(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
Zhang J.S., Xie C., Shen Y.G., Chen S.Y.;
Zhang J.S., Xie C., Shen Y.G., Chen S.Y.;
Zhang J.S., Xie C., Shen Y.G., Chen S.Y.;
Theo-component gene (NTHKI) encoding a putative ethylene receptor homolog is both developmentally and stress-regulated in tobacco.";
Theor. Appl. Genet. 102:815-824(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Serine/threonine kinase activity in the putative histidine kinase-like ethylane receptor NTHK1 from tobacco.";
Plant J. 33:385-393(2003).
-1- SIMILARITY: Contains 1 histidine kinase domain.
EMEL, APCS2627, ASC31213.3;
-1- SIMILARITY: TO1930.
HSSP, P49333; IDCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22444050; PubMed=12535351;
Xie C., Zhang J.S., Zhou H.L., Li J., Zhang Z.G., Wang D.W.,
Chen S.Y.,
                                                                                                                             01-07AY-1998 (TrEMBLrel. 05, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Ethylene receptor homolog.
                                                                                              762 AA.
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InterPro; IPR003661; His kinase.
InterPro; IPR009087; His kin homodim.
InterPro; IPR001089; Response_reg.
Pfam; PF02518; HATPase_c; 1.
                                                                                              PRT;
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Pfam; PF00072; Response_reg; 1.
ProDom; PD000039; Response_reg;
                                                                                              PRELIMINARY;
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MEDLINE=2036517; PubMed=10910347;
MEDLINE=2036517; PubMed=10910347;
MEDLINE=2036517; PubMed=10910347;
MEDLINE=2036517; PubMed=10910347;
MAIVATEDRA A.J. GAIRAN BAIONE G.S.,
MAIVATEDRA R.J., CAIRAN BAIONE M.R.S.,
MAIVATEDRA R.P., CAMARDO A.A., CAMARDO L.M., CATTATO D.M., FARGOR G.M., FRAGA J.S., FATROCA M.C., FORMER W., FUTIAN D.M., FRAGA J.S., FATROCA S.C., FRANCO M.C., Frohme M., Futlan D.R., Garnher M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gitualian J.P., ARTIGGER M., Lambais M.R., Leite D.C.C., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Madeira A.M.B.N., Madeira H.M.F., Maxino C.L.,
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
01-OCT-2003 (TremBlrel. 22, Last annotation update)
Cryza sativa (japonica cultivar-group).
01-NOTA sativa (japonica cultivar-group).
61-NATA SPERMATOPHYA; Magnoliophyta; Embryophyta; Poaceae;
62-NATA SPERMATOPHYA; Liliopsida; Poales; Poaceae;
63-NATA SPERMATOPHYA; NATA SPERMATOPHYA; NATA
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Xanthomonadaceae; Xylella.
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                                        2; Length 762;
                                             68.4%; Score 39; DB 2; Length 762
72.7%; Pred. No. 1.2e+02;
ive 0; Mismatches 3; Indels
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO03482; BAA78735.1; -.
Gramene, Q9XJ17; -.
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SEQUENCE 201 AA; 21230 MW; DDE198727729540B CRC64;
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Last annotation update)
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56.2%; Pred. No. 32;
tive 2; Mismatches
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97 TATVPHIGRAVPRRTR 112
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01-0CT-2000 (TEMBLrel. 15,
01-JUN-2003 (TEMBLrel. 24,
Hypothetical protein,
OrderedLocusNames=Xf1351;
Query Match
Best Local Similarity 72...
8; Conservative
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les 9; Conservative
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Nectria cinnabarina
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STRAIN=GJS 91-111;
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                 NCBI_TaxID=28549;
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Q7Q5V1;
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Q7Q5V1
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Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
A Menck C.F.M., Miracca B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netro L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Ouaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
de Slava A.C.R., da Silva A.M., da Silva A.J. Jr., de Souza A.D.Y.,
da Silva A.M., Massilva A.M., Jr., Savasaki H.E.,
da Silva A.C.R., Silva A.W., Variovski.-Almeida S., Vettore A.L.,
A. Sago M.A., Zatz M., Neidanis J., Setubal J.C.;
I.The genome sequence of the plant pathogen Xylella fastidiosa.";
I. Mature 406:151-159(2000)
I. Mature 406:151-159(2000)
I. REML; AR003967; AAF84160.1;
Complete proteome, Hypothetical protein.
SEQUENCE 42 AA, 4915 MW, 0F9B51F876FE0C9E CRC64;
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Diezmann S., Cox C.J., Schoenian G., Vilgalys R.J., Mitchell T.G.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX497608; AAT12528.1; -.
InterPro; IPR007645; RNA_pol_Rpb2_3.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
NCBI_TaxID=28549;
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20-MAY-2004 (TEEMBLrel. 27, Created)
20-MAY-2004 (TEEMBLrel. 27, Last sequence update)
20-MAY-2004 (TEEMBLrel. 27, Last annotation update)
20-MAY-2004 (TEEMBLrel. 27, Last annotation update)
RNA polymerase II second largest subunit (Fragment).
Debaryownyces carsonii.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Debaryomyces.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
RNA polymerase II second largest subunit (Fragment)
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STMPHQHRTR 26
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Best Local Similarity
7; Conserve
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nes 7; Conserv
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Name-agCG22391; ORFNames-ENSANGG0000018149;
Anopheles gambiae str. PEST.
EUKATYOCA; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
STRAIN=CBS 2285;
Discrann S., Cox C.J., Schoenian G., Vilgalys R.J., Mitchell T.G.,
"Molecular Phylogeny and Evolution of Candida and Related Species
Within the Order Saccharomycetales as Inferred From Multilocus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
                                                                                                                                                                                                                                                                                                         66.7%; Score 38; DB 2; Length 129; 70.0%; Pred. No. 25; 1; Indels iive 2; Mismatches 1; Indels
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY497608; AAT12528.1; -.
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                                                                                                                                                                                                                                                   129 AA; 14706 MW; 82AECOBID7D28326 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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05-071-2004 (TrEMBLrel. 27, Last sequence update)
05-071-2004 (TrEMBLrel. 27, Last annotation update)
NAN polymerase II subunit (Fragment).
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EMBL; AAAB01008960; BAA11578.1; -.
NON TER
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nes 7; Conservative
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59 TSNLQHVRRT 68
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86 SSTLSHLRRT 95
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Chaverri P., Castlebury L.A., Overton B.E., Samuels G.J.;

Thypocrea/Trichoderma: species with conidiophore elongations and green onidia...

Thypocrea/Trichoderma: species with conidiophore elongations and green onidia...

The Mycologia 95:1100-1140(2003).

BMBL, AF645567, AAQ11957.1;

TherPro; IPR007645; RNA_pol_Rpb2_3.

InterPro; IPR007645; RNA_pol_Rpb2_4.

InterPro; IPR007645; RNA_pol_Rpb2_4.

InterPro; IPR007645; RNA_pol_Rpb2_5.

Pfam; PF04565; RNA_pol_Rpb2_5.

Pfam; PF04565; RNA_pol_Rpb2_5; 1.

Pfam; PF04565; RNA_pol_Rpb2_5; 1.

Pfam; PF04567; RNA_pol_Rpb2_5; 1.

Pfam; PF04667; RNA_pol_Rpb2_5; 1.
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Search completed: November 10, 2004, 13:38:34 Job time : 14.4318 secs

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Sequence 15, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 45573, A
Sequence 45573, A
Sequence 45573, A
Sequence 64, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
                                                                                                                                                                             November 10, 2004, 12:32:37; Search time 4.14508 Seconds (without alignments) 191.991 Million cell updates/sec
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/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/8G_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 · Compugen Ltd
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US-09-098-079-18
US-09-088-079-18
US-08-811-519-25
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US-08-811-519-25
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US-09-270-767-61086
US-09-270-767-61086
US-09-270-767-61086
US-09-2108-452A-74
US-09-2108-452A-74
US-09-128-352-4688
US-09-128-352-4688
US-09-128-352-4688
US-09-128-352-4688
US-09-128-352-64
US-09-128-319-64
US-09-128-319-64
US-08-813-391-64
US-08-813-391-64
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 NGNLFASFIADS 12
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US-08-869-477-4
US-09-328-352-7248
US-08-142-328-32-7248
US-08-142-31603-16
US-08-453-956-25
US-08-453-956-25
US-08-453-956-25
US-09-631-603-17
PCT-US93-08174-25
US-09-631-10-4577
US-09-328-352-7237
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; Sequence 18, Application US/09097889
; Patent No. 6218117
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TOPOLOGY: linear
US-09-097-889-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
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Gaps

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RESULT 4
US-08-811-519-25
i Sequence 25. Application US/08811519B
patent No. 6630345
general Information:
APPLICANT: Petrenko, Alexandre
TITLE OF INVENTION: CHARACTERIZATION AND USES THEREOF
FILE REFRENCE: 1049-1-007
CURRENT APPLICATION NUMBER: US/08/811,519B
CURRENT FILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 31
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 4; Length 207;
Pred. No. 13;
2; Mismatches 0; Indels
                                                                                                                        Score 42; DB 4; Length 404;
Pred. No. 12;
                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-UW-453-956-15
Sequence 15, Application US/08453956
Patent No. 5770445
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION:
GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE 3. 25
CORRESPONDENCE AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
STATE: WA
COUNTRY: USA
COUNTRY: USA
COMPTRY: USA
COMPTRY: IBM PC COMPATIBLE
STATE: BADABLE FORM:
MEDIUM TYPE: FAODPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 18M PC COMPATIBLE
COMPUTER: 18M PC COMPATIBLE
COMPUTER: 18M PC COMPATIBLE
COMPUTER: 18M PC COMPATIBLE
COMPUTER: 18M PC COMPATIBLE
STATE: 30-MAY-1995
CLASSIFICATION NUMBER: US/08(453,956
FILING DATE: JUNY 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: US-WAN-1095
                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: McMasters, David D. REGISTRATION NUMBER: 33,963
                                                                                                                           Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19544
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Best Local Similarity 77.8-
                                                                                                                                                                                                                                                       1 NGNLFASFIADS 12
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Sequence 19544, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT FAPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PELING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 19544
LENGTH: 404
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                                                                                                    Sequence 18, Application US/09098079

Sequence 16, Application US/09098079

Patent No. 6489095

GENERAL INFORMATION:

APPLICANT: Herrnetadt, Corrina

APPLICANT: Fahy, Sounitra S.

APPLICANT: Fahy, Roin F.

APPLICANT: Pahy, Roin F.

APPLICANT: Davis, Roin F.

APPLICANT: APPLICANT: Davis, Roin F.

APPLICANT: APPLICANT: BATTON: EXTRAMITOCHONDDRIAL DNA
NUMBER OF SECUENCES: 26

CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 6.3;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA.

ZIP: 98104
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: ROSEMMAN PD. Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.416
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
FILEFRAX: (206) 622-4900
FILEFRAX: (206) 622-6031
FILEFRAX: (206) 622-6031
FILEFRAX: (206) 622-6031
FILEFRAX: C26 amino acids
LENGTH: 226 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NGNLFASFIA 10
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                                                                                             JS-09-098-079-18
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STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 40; DB 1; Length 485; 77.8%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:

COUNTRY: USA

ZUB: 99104-7092

ZUBI: 99104-7092

COMPUTER EARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRP PC COMPATIBLE
COMPUTER: IRP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/938,331
FILING DATE: J8-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTETCATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTETS, DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 39,9008.424C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/08086631
Patent No. 5776725
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Waylne R.
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
REFERENCE/DOCKET NUMBER: 990008.424C1
                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-624-4900
TELEPAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-956-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 HGNLFASFV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NGNLFASFI 9
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18-Sequence 15, Application US/0845230

PRETENT No. 591535

PRETENT NO. 591535

PRETENT NO. 591535

PRETENT SEATURE NO. 591535

PRESENCE ADDRESSES: SECONOMINATION REPROPER STREET: 600 COLUMBIA CENTER COURSESOURCE ADDRESSES: ADDRESSES: SECONOMINATION REPROPER STREET: 600 COLUMBIA CENTER COURSESOURCE ADDRESSES: SECONOMINATION REPROPER STREET: 600 COLUMBIA CENTER COURSESOURCE ADDRESSES: SECONOMINATION REPROPERTING STREET: 100 COLUMBIA CENTER COURTER STREET: 100 COLUMBIA CENTER STR
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Gaps

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Parent No. 67034 Application US/09270767

Parent No. 6703491

GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 45573

LENGTH: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37.5; DB 4; Length 311; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.0%; Score 39; DB 4; Length 148; 80.0%; Pred. No. 13; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                            Length 120;
                                                                                                                                                                                                                                          Score 39; DB 4;
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Xaa means any amino acid US-09-270-767-45573
    FILE REFERENCE: File Reference: 7326-094
CURRENT PEPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61086
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17937, Application US/09248796A
Patent No. 6747137
                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-61086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Drosophila melanogaster FEATURE:
                                                                                                                                                                                                                                            65.0%;
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83.3%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0.
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US-09-248-796A-17937
                                                                                                                                                                                                                                                                                                                                                                 13 NLFAAIIADS 22
                                                                                                                                                                                                                                                                                                                               3 NLFASFIADS 12
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41 NLFAAIIADS 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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US-09-270-767-45573
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APPLICANT:

APPLICANT:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT PELLING NUMBER: US,09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PELLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13377
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Sequence 61086, Application US/09270767

GENERAL INFORMATION:
APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08174
FILING DATE: 30-AUG-1993
CLASSIFICATION:
                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: JULY 1, 1993
APPLICATION NUMBER: 08/7/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCMASIGER, DAVIG D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008,424C1
TELEPHONE: 206-622-4900
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13377, Application US/09489039A Patent No. 6610836
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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49 SGTAFASFVGDS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein PCT-US93-08174-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 HGNLFASFV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-489-039A-13377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-039A-13377
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Gaps

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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: 05/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-03-13
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Score 35; DB 4; Length 330; Pred. No. 1.7e+02;

2; Mismatches

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Search completed: November 10, 2004, 13:44:07 Job time : 5.14508 secs
                                                                                                                                           58.3%;
                                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 6; Conservative
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2570
LENGTH: 330
                                                                                                                                                                                                                                                          117 GNSFSSFVRD 126
                                                              TYPE: PRT; ORGANISM: M.catarrhalis
US-09-540-236-2570
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Sequence 74, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffals, R.

APPLICANT: Griffals, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering the Perence of Invention and treatment of infection

TITLE OF INVENTION: and treatment of infection

TITLE REPRENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 74.

LENGTH: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2570, Application US/09540236

Patent No. 6673910
GENERAL INFORMATION:
FOR PAPELICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                 Sequence 4688, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER.
CURRENT APPLICATION NUMBER.
NUMBER OF SEQ ID NOS: 8252
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Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 377;
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60.0%; Score 36; DB 4; Length 377
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
      1; Indels
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      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4688
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; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-74
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Best Local Similarity 63.6
Matches 7; Conservative
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        10; Conservative
                                              1 NGNLFASFIADS 12
                                                                                      66 NANLFAS-IADS 76
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US-09-540-236-2570`
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US-09-328-352-4688
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US-09-198-452A-74
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4688
LENGTH: 377
        Matches
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RESULT 2
US-10-106-698-5361
Sequence 5361, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
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Matches 12; Conserv
12;
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Sequence 5361, Ap
Sequence 18, Appl
Sequence 192, App
Sequence 192, Appl
Sequence 2 Appl
Sequence 32727,
Sequence 32727,
Sequence 52549, A
Sequence 52549, A
Sequence 52849, A
Sequence 52849, A
Sequence 52849, A
                                                                                              November 10, 2004, 16:36:12; Search time 12.8912 Seconds (without alignments) 328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: \cgn2 6/ptodata/1/pubpaa/PCT_REW_DUB_Pep:*

2: \cgn2 6/ptodata/1/pubpaa/PCT_REW_DUB_Pep:*

3: \cgn2 6/ptodata/1/pubpaa/PCT_REW_DUB_Pep:*

4: \cgn2 6/ptodata/1/pubpaa/USO6_NEW_DUB_Pep:*

5: \cgn2 6/ptodata/1/pubpaa/USO6_NEW_DUB_Pep:*

6: \cgn2 6/ptodata/1/pubpaa/USO8_NEW_DUB_Pep:*

7: \cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB_Pep:*

8: \cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB_Pep:*

10: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

11: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

12: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

11: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

12: \cgn2 6/ptodata/1/pubpaa/USO8_NEW_PUB_PEP:*

13: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

14: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

15: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

16: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

17: \cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*

18: \cgn2 6/ptodata/1/pubpaa/USI0D_PUBCOMB_Pep:*

18: \cgn2 6/ptodata/1/pubpaa/USI0D_PUBCOMB_Pep:*

19: \cgn2 6/ptodata/1/pubpaa/USIND_PUBCOMB_Pep:*

10: \cgn2 6/ptodata/1/pubpaa/USIND_PUBCOMB_Pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-106-698-5361

4 US-10-106-698-592

4 US-10-106-698-592

4 US-10-408-759-18

6 US-10-408-758-192

7 US-10-010-065-2

7 US-10-425-115-186935

7 US-10-425-115-362727

6 US-10-425-114-52549

5 US-10-425-114-5255

5 US-10-425-114-5255

5 US-10-425-114-5255

5 US-10-425-114-3255

6 US-10-425-114-3255
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                                                                                                                                                                                                                                                                  1566620 seqs, 353225886 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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70.00
69.7
69.3
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Perfect score:
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044444666666
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Sequence 2344, Apple Sequence 135735, Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10922, Sequence 16922, Sequence 16922, Sequence 16310, Sequence 751, Appl Sequence 757, Appl Sequence 757, Appl Sequence 25172, Sequence 20112, Sequence 214913, Sequence 214913, Sequence 214913, Sequence 214913, Sequence 214913, Sequence 21781, Sequence 21776, Sequence 21781, Sequence 21781, Sequence 21781, Sequence 333, Appl
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                   Sequence 210244,
Sequence 209563,
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Sequence 35, Application US/10092750

Sequence 35, Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: MISHI, Martin C.
TITLE REFERENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT PELLORION NUMBER: US 60/274,526

PRIOR PPLIAGO DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 12
7 US-10-739-930-8886

5 US-10-424-599-210244

6 US-10-437-959-210244

6 US-10-437-953-135735

6 US-10-632-585-7313

5 US-10-632-585-7313

5 US-10-632-585-7313

5 US-10-632-1537-100

10-424-599-169281

6 US-10-437-963-169281

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10S-10-2806-751

10S-10-425-115-291781

10S-10-425-115-291781

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10S-10-425-114-47512

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     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-092-750-35
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Gaps
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Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Tahay, Bing
APPLICANT: Glosh, Sumitra S.
APPLICANT: Glosh, Bang
APPLICANT: Glosh, Bang
APPLICANT: Glosh, Gary M.
APPLICANT: Warnock, Dale E.
APPLICANT: Warnock, Dale E.
APPLICANT: Warnock, Dale E.
APPLICANT: Glosh, Gary M.
APPLICANT: Glosh, Ga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 9; Length 226; Pred. No. 10; Mismatches 1; Indels
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
CONFUTER: LORDY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-UN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: ROSENMAN DH.D., Stephen J.
REGISTRATION NUMBER: 43.058
REFERENCE/DOCKET NUMBER: 660089.416
TELEPHONE: (200) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2.26 amino acids
TYPE: amino acids
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Best Local Similarity 90.0%
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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US-09-098-079-18
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Sublication No. US20030109690A1
GENERAL INFORMATION:
TITLE OF INVENTION:
GENERAL APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2000-09-28
FRIOR FILING DATE: 2000-09-28
FRIOR FILING DATE: 1999-09-29
FRIOR FILING DATE: 1999-09-29
FRIOR FILING DATE: 1999-19-29
FRIOR FILING DATE: 1999-19-29
FRIOR FILING DATE: 1999-19-29
FRIOR FILING DATE: 1999-11-03
       APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polymuclectides and Polypeptide FILE REPERENCE: PAGGSP1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1090-09-28
PRIOR FILING DATE: 1990-09-29
PRIOR PRILING DATE: 1999-09-10-30
RIGHT PRILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
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Ratent No. US200200064733A1

GENERAL INFORMATION:

APPLICANT: Herrnstadt, Corrina

APPLICANT: Ghosh, Scumitra S.

APPLICANT: Clevenger, William

APPLICANT: Fahy, Boin F.

APPLICANT: Fahy, Roin F.

ATTILE OF INVENTION: BARTRAMITOCHONDBRIAL DNA

TITLE OF INVENTION: EXTRAMITOCHONDBRIAL DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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Pred. No. 2.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-10-106-698-5361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-10-106-698-6592
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US-10-106-698-6592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5361
LENGTH: 53
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LENGTH: 58
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US-09-098-079-18
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Sequence 362727, Application US/10425115
; Sequence 362727, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
; APPLICANT: David K.
; APPLICANT: David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION PLANTS
; TITLE OF INVENTION NUMBER: US/10/425,115
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT PILING DATE: 2003-04-28
; SEQ ID NOS 362227
; LEMBER OF SEQ ID NOS: 369326
; SEQ ID NO 362227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORCANISM: Zea may8
FEATURE:
NAME/KEX: unsure
LOCATION: (1)..(85)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_93981C.1.pep
US-10-425-115-362727
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Best Local Similarity 50.0
Matches 6; Conservative
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-437-963-141470
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Sequence 18693
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                                                                                                                                                                    Sequence 2, Application US/10010065

Publication No. US20020144300A1

GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
APPLICANT: Allen, Keith D.
APPLICANT: Moore, Wark
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING GLUCAGON
TITLE OF INVENTION: RECEPTOR GENE DISRUPTIONS
FILE REFERRINCE: R-648
CURRENT FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR PAPLICATION NUMBER: US 60/266,044
PRIOR FILING DATE: 2001-02-01
PRIOR PELING DATE: 2001-02-01
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
LENGTH: 485
TAVER: DATE
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LOCATION: (1)...(79)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

FOATURE: INFORMATION: Clone ID: MRT4577_102073C.1.pep

US-10-425-115-186935
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Matches 7; Conservative
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ORGANISM: Mus musculus
US-10-010-065-2
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ORGANISM: Zea mays
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Sequence 144470, Application US/10437963
; Sequence 144470, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Li, Ping
; APPLICANT: Boukharov, Li, Ping
; TILLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TILLE OF INVENTION: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 14470
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                                                      Gaps
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63.3%; Score 38; DB 17; Length 85; 50.0%; Pred. No. 20; ive 4; Mismatches 2; Indel8
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US-10-437-963-141470
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US-10-425-114-52549
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| ||||||| 2 NENLFASFI 10

RESULT 8

Sequence 52549, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:

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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Sovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cor INVENTION: Mucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 43548
LENGTH: 527
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Sequence 8886, Application US/10739930

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: 18-21 (53377) B
CURRENT FILING DATE: 2003-12-18
CURRENT FILING DATE: 2003-12-18
SEQ ID NO 8886
LENGTH: 527
                       APPLICANT: Cao, Yongwei Title OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NOS: 73128 LENGTH: 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.3%; Score 38; DB 15; Length 327; Best Local Similarity 72.7%; Pred. No. 88; Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.3%; Score 38; DB 15; Length 52772.7%; Pred. No. 1.5e+02;
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US-10-425-114-52852
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CRGANISM: Glycine max
FATURE:
FATURE:
CONTRACTON: Clone ID: 700726816_FLI.pep
US-10-425-114-43548
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Sequence 43548, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:
Tabaska, Jack E
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 NGNLKTSFCAD 228
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                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
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US-10-739-930-8886
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Publication No. US20040072774A1
GENERAL INFORMATION:
APPLICANT: COLUMBIA UNIVERSITY
APPLICANT: Manfredi, Glovanni
APPLICANT: Schon, Eric
TITLE OF INVENTION: METHODS FOR EXPRESSING AND TARGETING MITOCHONDRIA-DNA-ENCODED
TITLE OF INVENTION: PEPTIDES AND USES THEREOF
FILE REFERENCE: 5199-6
CURRENT APPLICATION NUMBER: US/10/371,592
CURRENT APPLICATION NUMBER: US 60/358,935
PRIOR PILING DATE: 2002-02-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 2
                                                                           APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Seeven E
APPLICANT: Screen, Seeven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Seeven E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO S2549
LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.3%; Score 38; DB 15; Length 222; 72.7%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: LIB3028-051-H9_FLI.pep
US-10-425-114-52549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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US-10-425-114-52852
US-10-425-114-52852
Sequence 5852, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Xovalic, David K.
APPLICANT: Screen, Steven E
```

Best Local Similarity 72.7 Matches 8; Conservative

Query Match

TYPE: PRT ORGANISM: Glycine max

FEATURE:

JS-10-371-592-2

TYPE: PRT) ORGANISM: Homo sapiens US-10-371-592-2

3 NLFASFIA 10 |||||||| 67 NLFASFIA 74

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Query Match Best Local Similarity Matches 8; Conserv

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RESULT 15

US-10-424-599-210244

IS-quence 210244, Application US/10424599

Fublication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Vongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5323)B

CURRENT APPLICATION UNMERR: US/10/424,599

CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 285684

ENERGY FILING STATA

SEQ ID NO 210244
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                                                                                                                                           Query Match 63.3%; Score 38; DB 17; Length 527; Best Local Similarity 72.7%; Pred. No. 1.5e+02; Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.3%; Score 38; DB 15; Length 645; Best Local Similarity 72.7%; Pred. No. 1.8e+02; Matches 8; Conservative 0; Mismatches 3; Indels
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LOCATION: (1)..(645)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_31879C.1.pep

US-10-424-599-210244
; TYPE: PRT ; ORGANISM: Glycine max ; FEATURE: ; PEATURE: ; OTHER INFORMATION: Clone ID: GLYMA-23APR03-C2174_9.p US-10-739-930-8886
                                                                                                                                                                                                                                                                               418 NGNLKTSFCAD 428
                                                                                                                                                                                                                                         1 NGNLFASFIAD 11
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Search completed: November 11, 2004, 01:28:17 Job time : 13.9412 secs

536 NGNLKTSFCAD 546

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GenCore version 5.1.6
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- protein search, using sw model OM protein November 10, 2004, 12:29:32; Search time 2.67358 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

US-10-092-750-35 Title:

1 NGNLFASFIADS 12 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	H+-transporting tw	H+-transporting tw	H+-transporting tw	H+-transporting tw	glucagon receptor	glucagon receptor	H+-transporting tw	H+-transporting tw	H+-transporting tw	H+-transporting tw	cobalamin biosynth	phosphate uptake A	potassium-transpor	potassium-transpor	zinc-finger protei	H+-transporting tw	TcaB protein [impo	probable ThrC2 thr	ribosomal protein	site-specific DNA-	carboxylesterase,	phosphomannomutase	phosphomannomutase	cation efflux syst	H+-transporting tw	H+-transporting tw	Qu	oxidoreductase ycg	hypothetical prote
SUMMARIES	ID	PWHU6	F59153	T10977	T11498	JC4363	JQ1957	PWMS6	T11145	T11055	804752	D90153	H95946	A11409	AH1785	T18297	T37052	F90035	G95293	S78395	S02856	A75250	A72124	A86498	96	급	25	T48166 .	86	H72683
	DB																											N		
	Query Match Length	226	226	226	226	485	485	226	226	226	226	293	505	561	561	1151	166	402	484	220	403	540	598	598	1166	226	226	307	357	394
æ	Query Match	70.0	70.0	70.0	66.7	66.7	66.7	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	61.7	61.7	61.7	60.09	60.0	60.0	60.09	60.0	0.09	58.3	58.3	58.3	58.3	58.3
	Score	42	42	42	40	40	40	38	38	38	38	38	38	38	38	38	37	37	37	36	36	36	36	36	36	35	35	35	35	35
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probable transposa	hypothetical prote	F25A4.24 [imported	beta-fructofuranos	oge	semaphorin I precu	hypothetical prote	hypothetical prote	H+-transporting tw	_	5 E	_	transporting (transporting 1	H+-transporting tw	H+-transporting tw
T36649	F82354	C96777	T12083	T06560	A49423	828700	B65045	PWBO6	T11446	T11407	S41840	826156	T11368	T11862	T11252
N	N	N	~	N	(7)	N	N	н	N	7	~	~	0	0	N
407	436	642	651	672	711	137	. 210	226	226	226	226	226	226	226	226
58.3	58.3	58,3	58.3	58.3	58.3	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7
35	35	35	35	32	35	34	34	34	34	34	34	34	34	34	34

ALIGNMENTS

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	RESULT 1 PWHUS
	H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - human mitochondrion N:Alternate names: hydrogen ion-transporting ATP synthase protein 6
	C. Species: mitochondrion Homo sapiens (man)
	C;Date: 22-May-1981 #Bequence_revision 23-Oct-1981 #text_cnauge 09-our-2004 C;Accession: A01049
	R; Anderson, S.; Bankier, A.T.; Barrell, B.G.; de Bruijn, M.H.L.; Coulson, A.R.; Drouin,
	Nature 290, 457-465, 1981
	Aritle: Sequence and organization of the human mitochondrial genome.
	A;Accession: A01049
	A, Molecule type: DNA
	A; Regidues: 1-226 <and></and>
	A.//COMBETERENCES: UNIFRCO.:FOUGAS) GB:UNIALSTO, GB:UNIALSTO, GB:UNIOCOL, GL:UNIOLSTO, GB:UNIOLSTO, GB:UNIOLS
	A.Gene: GDB:MTATP6
	A;Cross-references: GDB:118897; OMIM:516060
	A,Map position: MTH8527-9207
	A, Genome: mitochondrion
	A,Genetic code: SGC1
	C; Superfamily: H+-transporting ATP synthase protein 6
	C; Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mirochondrion; oxid
	70.0%;
	Best Local Similarity 90.0%; Pred. No. 2; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
	Qy 1 NGNLFASFIA 10
	DB 2 NEWLFASFIA 11

2 NENLFASFIA 11

RESULT 2

H-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - western lowland gorilla mitor N;Alternate names: hydrogen ion-transporting ATP synthase protein 6 C;Species: mitochondrion Gorilla gorilla (western lowland gorilla) C;Species: mitochondrion Gorilla gorilla (western lowland gorilla) C;Accession: F59153
B;Xu, X.; Arnason, U.
Mol. Biol. Evol. 13, 691-698, 1996
A;Title: A complete sequence of the mitochondrial genome of the Western lowland gorilla. A;Reference number: Z17269; MUID:96212991; PMID:8676744
A;Accession: F59153
A;Accession: F59153
A;Molecule type: DNA
A;Residues: 1-226 < xUX>
A;Accession: Kype: DNA
A;Residues: 1-226 < xUX>
A;Residues: 1-226 < xUX>
A;Accession: MUIPROT:Q9T977; GB:X93347; NID:g1304307; GSPDB:GN00106
A;Cross-references: UNIPROT:Q9T987; GB:X93347; NID:g1304307; GSPDB:GN00106
A;Note: submitted to GenBank, November 1995
A;Note: this translation is not annotated in GenBank entry GGMITG, release 114.0

C;Genetics:

D 8

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A; Title: The complete nucleotide sequence of the domestic dog (Canis familiaris) mitochor A; Reference number: 217276; MUID:99097286; PMID:9878232
A; Accession: Title: Muid: 217276; MUID:99097286; PMID:9878232
A; Accession: Title: Muid: 217276; Muid: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Genome: mitochondrion
A Genetic ode: 8GC1
C,Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT: Q61606; GB: L38612; NID: 97274387; PIDN: AAF44749.1; PID: 9727438 C; Comment: This receptor is a plasma membrane glycoprotein that belongs to a subfamily of epolysis and gluconeogenesis in li ver and insulin secretion by beta cells. C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucagon receptor - rat
N;Alternate names: GLP-1 receptor homolog, hepatic
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1957; A46211; S29689
R;Svoboda, M.; Ciccarelli, E.; Tastenoy, M.; Cauvin, A.; Stievenart, M.; Charistophe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: JC4363
R;Burcelin, K.; Li, J.; Charron, M.J.
Gene 164, 305-310, 1995
A;Title: Cloning and sequence analysis of the murine glucagon receptor-encoding gene.
A;Reference number: JC4363; MUID:96069600; PMID:7590348
A;Accession: JC4363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-Feb-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 40; DB 2; Length 226; llarity 75.0%; Pred. No. 4.8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 485;
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Mol. Phylogenet. Evol. 10, 210-220, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Mus musculus (house mouse)
Date: 08-Jan-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucagon receptor precursor - mouse C; Species: Mus musculus // Amana musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NGNLFASFIADS 12
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178 HGNLFASFV 186
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Best Local Similarity
Matches 9; Conserv
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Matches 7; Conserv
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A; Residues: 1-485 <BUR>
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                                                                                 A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - pig mitochondrion Cispecies: mitochondrion Sus scrofa domestica (domestic pig) C;Species: mitochondrion Sus scrofa domestica (domestic pig) C;Date: 16-Jul-1999 #sequence-revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T10977; T11875; A45954 R;Lin, C.S.; Liu, C.Y.; Sun, Y.L.; Chang, L.C.; Cheng, I.C.; Yang, P.C.; Mao, S.J.T.; Hu submitted to the EMBL Data Library, November 1997 A;Bescription: Complete nucleotide sequence of the porcine mitochondrial genome. A;Accession: T10977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: i-226 «LIN»
|Cross-references: UNIPROT:Q35915; EMBL:AF034253; NID:g4958951; PID:g4958957; PIDN:AAD3
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A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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Watanabe, T.; Hayashi, Y.; Kimura, J.; Yasuda, Y.; Saitou, N.; Tomita, T.; Ogasawara, Jochem. Genet. 24, 385-396, 1986

Filtle: Pig mitochondrial DNA: polymorphism, restriction map orientation, and sequence in the second map or second sequence is the second map or second second map or second second second map or second sec
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ubmitted to the EMBL Data Library, February 1999
ubmitted to the EMBL Data Library, February 1999
upmitted to the EMBL Data Library, February 1999
upmitted to the pig (Sus scrofa).
y,Reference number: Z17370
u:Accession: T11875
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H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - dog mitochondrion
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C;Date: 16-101-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T1498
R;Kim, K.S.; Lee, S.E.; Jeong, H.W.; Ha, J.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                 70.0%; Score 42; DB 2; Length 226; larity 90.0%; Pred. No. 2; Conservative 0; Mismatches 1; Indels
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Molecule type: DNA
Residues: 1-226 <URS>
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Residues: 1-28;219-226 <WAT>
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Best Local Similarity
Matches 9; Conserv
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                                                      A; Gene: ATPase6
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Genetics:

Best Loc Matches

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H-transporting two-sector ArPase (EC 3.6.3.14) protein 6 - fruit bat (Artibeus jamaicens C,Species: mitochondrion Artibeus jamaicensis
C,Species: mitochondrion Artibeus jamaicensis
C,Species: mitochondrion Artibeus jamaicensis
C,Accession: T1145
R,Pumo, D.E.; Finamore, P.S.; Franek, W.R.; Phillips, C.J.; Tarzami, S.; Balzarano, D. J. Mol. Evol. 47, 709-717, 1998
A,Fittle: Complete mitochondrial genome of a neotropical fruit bat, Artibeus jamaicensis, A,Accession: T1145
A,Accession: T1145
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A,Accession: T1145
A,Accession: T1145
A,Molecule type: DNA
A,Residues: 1-226 cPUM>
A,Gorderics: UNIPROT:099599; EMBL:AF061340; NID:g4164474; PID:g4164480; PIDN:AADOF
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C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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840452
H-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - rat mitochondrion
C;Species: mitochondrion Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-
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A;Retues: Dreliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Residues: 1-37, W',38-215, W',217-323, V',325-485 <JEL>
A;Reperfameral source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:127785)
C;Genetics:
A;Introns: 133/3; 168/2; 220/3; 407/3
C;Reywords: G protein-coupled receptor
C;Reywords: G protein-coupled receptor
F;144-167/Domain: transmembrane #status predicted <TM2>
F;175-194/Domain: transmembrane #status predicted <TM4>
F;267-221/Domain: transmembrane #status predicted <TM4>
F;264-226/Domain: transmembrane #status predicted <TM4>
F;264-226/Domain: transmembrane #status predicted <TM6>
F;365-324/Domain: transmembrane #status predicted <TM6>
F;365-324/Domain: transmembrane #status predicted <TM6>
F;365-405/Domain: transmembrane #status predicted <TM6>
F;389-405/Domain: tran
                                A,Title: Small introns in a hepatic cDNA encoding a new glucagon-like peptide 1-type red A,Reference number: JQ1957; MJID:93213282; PMID:8384842
A,Accession: JQ1957; MJID:93213282; PMID:8384842
A,Accession: JQ1957
A,Molecule type: mRNA
A,Residues: 1-485 <SVO.
A,FResidues: 1-485 <SVO.
A,FResidues: 1-485 <SVO.
A,FResidues: 1-485 <SVO.
A,FResidues: 1-485 <SVO.
A,FRepermental source: liver
R,Jelinek, L.J.; Lok, S.; Rosenberg, G.B.; Smith, R.A.; Grant, F.J.; Biggs, S.; Bensch, Science 259, 1614-1616, 1993
A,Title: Expression cloning and signaling properties of the rat glucagon receptor.
A,Reference number: A46211; MJID:93206096; PMID:8384375
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A;Genetic code: SGG:
C:Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthssis; hỳdrolase; membrane-associated complex; mitochondrion;
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Biochem. Biophys. Res. Commun. 191, 479-486, 1993
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Pred. No. 11;
2; Mismatches
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 8; Conserv
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Gaps .; 0

A; Genome: mitochondrion

Genetics:

A;Residues: 1-226 <GAD>

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potassium-transporting atpase a chain homolog kdpA [imported] - Listeria monocytogenes (s) Species: Listeria monocytogenes (c) Species: Listeria monocytogenes (c) Species: Listeria monocytogenes (c) Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 (c) Accession Alidop Al
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Modecule type: DNA
A,Residues: 1-561 <GLA>
A,Cross_references: UNIPROT:Q8<u>Y3</u>26; GB:NC_003210; PIDN:CAD00895.1; PID:g16412182; GSPDB:C
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A,Molecule type: DNA
A,Residues: 1-561 GCLA-
A,Cross-references: UNIRROT:Q927F9; GB:AL592022; PIDN:CAC98056.1; PID:g16415365; GSPDB:GN
A,Experimental source: strain Clip11262
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R;Glaser; P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A;Authors: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C,Species: Listeria innocua
C,Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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                                                                                                                                  63.3%; Score 38; DB 2; Length 505; 88.9%; Pred. No. 27; tive 0; Mismatches 1; Indels
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C; Genetics:
A; Gene: KdpA
C; Superfamily: H+/K+-exchanging ATPase subunit A
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Best Local Similarity 58.39
Matches 7; Conservative
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                                                                                                                                  Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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A; Gene: phoT; SMb21174
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                                                          A; Genome: plasmid
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                                                     A, Cross-references: UNIPROT: P05504; EMBL: X14848; NID: 9854269; PIDN: CAA32959.1; PID: 91346
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A;Status: preliminary
A;Modecule type: DNA
A;Residues: 1-293 <KCR>
A;Cross-references: UNIPROT:Q980Y9; GB:AE006641; NID:g13813263; PIDN:AAK40483.1; GSPDB:G
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A;Notecule type: DNA
A;Nolecule type: DNA
A;Rosidues: 1-50S < KUR>
A;Cross-references: UNIPROT: Q52909; GB:AL591985; PIDN: CAC49240.1; PID:g15140726; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSym3
R;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P:; Federspiel, N.A.; Fisher, R.F.;
Bcience 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Reference number: A$6039; WUID:21368234; PMID:11474104
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C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc
A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: D90153 Fragatanieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Kr;She, O.; Sindh, R.K.; Confalanieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Sensen, M.A.; Sensen, C.W.; Van der Oost, J. A.; April 2001
A;Description: Sulfolobus solfataricus complete genome.
A)Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cobalamin biosynthesis protein G (cbiG) [imported] - Sulfolobus solfataricus
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
                                                                                                                                                                                         Ouery Match 63.3%; Score 38; DB 2; Length 226; Best Local Similarity 88.9%; Pred. No. 11; Matches 8; Conservative 0; Mismatches 1; Indels
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Local Similarity 63.0

Best Loc Matches

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Db

Query Match

A, Gene: cbiG

C; Genetics

Accession: D90153

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C; Genetics:

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1 NGNLFASFIADS 12 ||:|| ||: 468 NGSAFAGFAADT 479 셤

Cispecies: Mus musculus (house mouse)
Cispecies: Is-Oot-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cispecies: Is-Oot-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cispecies: Is-Oot-1999 #sequence_revision 18-Oct-1999 #text_change 09-Jul-2004
Cispecies: Is-Oot-1999 #sequence Indianaly Indianaly Indianaly Indianaly PMID: 9927674
Aignosion: Indianaly translated from GB/EMBL/DDBJ
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Gaps ö Query Match 63.3%; Score 38; DB 2; Length 1151; Best Local Similarity 70.0%; Pred. No. 63; Matches 7; Conservative 2; Mismatches 1; Indels

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1 NGNLFASFIA 10 |||||:|:| 928 NGNLFSSHLA 937

Search completed: November 10, 2004, 13:40:43 Job time : 3.67358 secs

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homo sapien
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homo sapien
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SEQUENCE FROM N.A.

STRAIN=RIMD 2210633 / Serotype 03:K6;

XX MEDINES=22508454; PubMed=12620739;

XA MEDINES=22508454; PubMed=12620739;

AN ARAINO K., Coshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

XA Ijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

XA Isima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

XA Isima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

XA Isima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

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XA Isima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

XA Isima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

XA Isima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

XI Inacer J. 17001001000 parahaemolyticus: a pathogenic mechanism Go, Go: 0003024; Procelysis and peptidolysis; IEA.

DR GO, GO: 000508; P:procelysis and peptidolysis; IEA.

RO; GO: 000508; P:procelysis and peptidolysis; IEA.

RO; GO: 000508; P:procelysis and peptidolysis; IEA.

RICEPPO: IPRO01375; Peptidase—59A.N.

RICEPPO: IPRO01375; Peptidase—59A.N.

RICEPPO: IPRO01379; Peptidase—59A.N.

RICEPPO: IPRO013799; Peptidase—59A.N.

RICEPPO: IPRO01379; Peptidase—59A.N.

RICEP
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Q71j27
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07ycd1
07ycf8
07ycf8
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-COT-2003 (TrEMBLrel. 25, Last annotation update)
01-JUN-2005 (TrEMBLrel. 25, Last annotation update)
02-Cotor and parahaemolydicus.
02-Cotor annotation parahaemolydicus.
03-Cotor annotation para
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Pred. No. 20;
2; Mismatches 1; Indels
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PROSITE; PS007708; PRO_ENDOPEP_SER; 1.
Complete protecme.
SEQUENCE 754 AA; 84245 MW; 65EF726912510A02 CRC64;
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Q6VLP4
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Q714Z4
Q71K48
Q77K86
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(c) 1993 - 2004 Compugen Ltd.
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ATP synthase a chain (EC 3.6.3.14) (ATPase protein Name=MTATP6; Synonyms=ATP6; Homo sapiens (Human). Mitochondrion.
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Am. J. Hum. Genet. 46:428-433(1990)
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VARIANT NARP ARG-156.
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Mammalia; Butheria; Cetartiodactyla, Suina; Suidae, Sus.
NCBI_TaxID=9823;
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                         SEQUENCE FROM N.A.
TISSUB=Peripheral blood;
MEDLINE=98403943; PubMed=9734874;
MEDLINE=98403943; PubMed=9734874;
Tartaglia M., Saulle E.;
"Rapid communication: nucleotide sequence of porcine and ovine tRNA(Lys) and AFPase8 mitochondrial genes.";
J. Anim. Sci. 76:2207-2208(1998).
EMBL; AF039179; AB05065.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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TISSUB=peripheral blood;
MEDLINE=9840343; PubMed=9734874;
Tartaglia M., Saull E.;
"Rapid communication: nucleotide sequence of porcine and ovine tRNA[tys) and ATPRase8 mitochondrial genes.";
J. Anim. Sci. 76;2207-2208 (1998);
EMBL; AF039170; AAD05065.1;
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0; Mismatches 1; Indels
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SEQÜENCE 22 AA; 2411 MW; D440C56CAE0EAIC9 CRC64;
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    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATPase subunit 6 (Fragment).
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Last annotation update)
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ATPase subunit 6 (Fragment).
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Matches
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RESULT 3

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TISSUE=Placenta;
MEDLINE=95132634; PubMed=7530363;
Horal S., Hayasaka K., Kondo R., Tsugane K., Takahata N.;
"Recent African origin of modern humans revealed by complete sequences of hominoid mitochondrial DNAs.";
Proc. Natl. Acad. Sci. U.S.A. 92:532-536(1995).
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MEDLINE=22062553; PubMed=12022039;
Silva W.A. Jr., Bonatto S.L., Holanda A.J., Ribeiro-Dos-Santos A.K.,
Barkao B.M., Goldman G.H., Abe-Sandes K., Rodriguez-Deifin L.,
Barkaos M., Paco-Larson M.L., Petzl-Erler M.L., Valente V.,
Santos S.E., Zago M.A.;
Mitochondrial genome diversity of native Americans supports a single early entry of founder populations into America.";
Am. J. Hum. Genet. 71:187-192(2002).
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MEDDINE-89072713; PubMed=3201231;
Wallace D.C., Singh G., Lott M.T., Hodge J.A., Schurr T.G.,
Lezza A.W., Elsas L.J. II, Nikoskelainen E.K.;
"Mitochondrial DNA mutation associated with Leber's hereditary optic
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Lamminen T., Majander A., Juvonen V., Wikstroem M., Aula P.,
Nikoskelainen E., Savontaus M.-L.;
"A mitochondrial mutation at nt 9101 in the ATP synthase 6 gene
associated with deficient oxidative phosphorylation in a family with
Leber hereditary optic neuroretinopathy.";
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILIE-8117022; PubMed=7219534;
MEDILIE-8117022; PubMed=7219534;
Anderson S., Bankier A.T., Barrell B.G., de Bruijn M.H.L.,
Coulson A.R., Drouin J., Eperon I.C., Nierlich D.P., Roe B.A.,
Sanger F., Schreier P.H., Smith A.J.H., Staden R., Young I.G.;
"Sequence and organization of the human mitochondrial genome.";
Nature 290:457-465(1981).
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MEDILMES9331018; PubMed=8295787;
de Vries D.D., van Engelen B.G.M., Gabreels F.J.M., Ruitenbeek
van Oost B.A.;
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Holt I.J., Harding A.E., Petty R.K., Morgan-Hughes J.A.;
"A new mitochondrial disease associated with mitochondrial DNA
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/FTId=VAR_008557.
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EMBL; AF465862; AAN14772.1; --.
PIR; A01049; PWHUG.
Genew; HGNC:7414; MIATP6.
MIM; 516060; --.
MIM; 516060; --.
    EMBL; J01415; AAB58948.1; -.
EMBL; V00662; CAA24031.1; -.
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MIM; 256000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIESTANE: MEDITION MATERIA AND THE ARE THE CAUSE OF NEUROSCIE.

WEARNESS, ALAXIA, AND TETINITIS PIGMENTOSA (NARP) [WIM:551500].

DISEASE: Defects in WIATPG are a cause of Leber's hereditary optic neuropathy (LHON) [MIM:555000], also known as Leber's optic atrophy. LHON is a maternally inherited disease resulting in acute blindness due to retinal degeneration predominantly in young man. Cardiac conduction defects and neurological defects have also been described.

DISEASE: Defects in MIATPG are a cause of Leigh syndrome (LS) [MIM:256000]. LS is a severe neurological disorder characterized by bilaterally symmetrical necrotic lesions in subcortical brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT LS PRO-217.
MEDLINE=98161883; PubMed=9501263;
Dionial-Vici C., Seneca S., Zeviani M., Fariello G., Rimoldi M.,
Bertini E., De Meirleir L.;
"Fulminant Leigh syndrome and sudden unexpected death in a family with
the T9176C mutation of the mitochondrial ATPase 6 gene.";
J. Inherit. Metab. Dis. 21:2-8(1998).
Am. J. Hum. Genet. 56:1238-1240(1995).

[9]
VARIANT FESN PRO-217.
MEDLINE=95398422; PubMed=7668837;
MEDLINE=95398422; PubMed=7668837;
MEDLINE=95398422; PubMed=7668837;
MEDLINE=95398422; PubMed=7668837;
MEDLINE=95398422; PubMed=7668837;
MEDLINE=9539842; PubMed=7668837;
MEDLINE=9539842; PubMed=7668837;
MEDLINE=9539842; PubMed=7688437;
MEDLINE=9539842; PubMed=7688437;
MEDLINE=95398437;
MEDLINE=95398427;
MEDLINE=9539847;
MEDL
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SUBUNIT: F. type ArPases have 2 components, CF(1) - the catalytic SUBUNIT: and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.

SUBCELLUIAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT THR-155.
MEDLINE=89127994; PubMed=9461455;
Rieder M.J., Taylor S.L., Tobe V.O., Nickerson D.A.;
Rieder M.J., Taylor S.L., Tobe D.O., Nickerson D.A.;
Automating the identification of DNA variations using quality-based fluorescence re-sequencing: analysis of the human mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE 99220421; PubMed=9556461; Takahashi S., Makita Y., Oki J., Miyamoto A., Yanagawa J., Naito B., Goto Y., Okuno A.; Takahashi S., Makita Y., Oki J., Miyamoto A., Takahashi S., Makita Y., Okuno A.; Maritation resulting in Leigh syndrome."; Am. J. Hum. Genet. 62:717-719(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome.";

Nucleic Acids Res. 26:967-973(1998).

Nucleic Acids Res. 26:967-973(1998).

-!- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane.

-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +

-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: Defects in WTATP6 may be a cause of familial bilateral striatal necrosis (FBSN). FBSN is a neurological disorder resembling Leigh syndrome.
                                                                                                                                                                                                    MEDLINE=9741664; PubMed=9270604; Campos Y., Martin M.A., Rubio J.C., Solana L.G., Garcia-Benayas C. Tarradas J.L., Arenas J.;
"Leigh syndrome associated with the T9176C mutation in the AFPase gene of mitochondrial DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the ATPase A chain family.
                                                                                                                                                  Ann. Neurol. 38:468-472(1995).
                                                                                                                                                                                                                                                                                                                                                                 VARIANT LS ARG-156.
                                                                                                                                                                                           PRO-217
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/FTId=VAR_008561.
T -> T (in_LHON; possible rate primary
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823,
                                                                Pfam; PF00119; ATP-synt As; 1.

PRINTS; PR00123; ATP-synt As; 1.

TIGRPAMS; TIGR01131; ATP-synt 6 or A; 1.

PROSITE; PS0049; ATPASE A; 1.

CF(0); Disease mutation; Hydrogen ion transport;

CF(0); Disease mutation; Hydrogen ion transport;

Polymorphism; Transmembrane. T -> S.

VARIANT
MIM; 256000; -. Governon-transporting ATP synthase complex, C. GO; GO:00015986; P:ATP synthesis coupled proton transport; NAS. InterPro; IPR000568; ATPsynt_Asub.
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Pred. No. 14;
0; Mismatches 1; Indels
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
ATE synthase a chain (EC 3.6.3.14) (ATPase protein 6).
Name-MTATP6; Synonyms-ATF6, ATPASE6;
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LS)
                                                                                                                                                                                                                                                                                                                                                                                                                                       A -> T.

/FIIdeVAR 008560.

L -> R (in NAEP and L.

/FIIdeVAR 000793.

L -> P (in LS).

/FIIdeVAR 000794.
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L -> P (in LS and in
striatal necrosis).
/Frid=VAR_000797.
S -> G.
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ATP6_PIG
AC Q35915; O7
DT 15-DEC-199
DT 05-JUL-200
DE ATP SYNTHA
GN Name=MTATP
OG Mitochondr
OC Bukaryota;
OC Mammalla;
OX NOBI_TAXID
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114 (1014). The Arpases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunites: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunites: alpha(3), pamma(1), delta(1), epsilon(1). CF(0) has three main subunites: alpha(3), pamma(1), delta(1), epsilon(1). CF(0) co. SUBCELBULAR LOCATION: Integral membrane protein (By similarity).

1. SIMILARITY: Belongs to the ATPase A chain family. Remain, PAS19486; AAR91237.1; -..

2. SIMILARITY: Belongs to the ATPase A chain family. Remain, PRO0119; ATP-Synt Asub.

2. PRIMTS: PRO0129; ATP-Synt Asub.

3. TIGRFAMS: TIGRO1131; ATP-Synt Gor A; 1.

4. TIGRFAMS: TIGRO1131; ATP-Synt Gor A; 1.

5. TIGRFAMS: TIGRO1131; ATP-Synt Gor A; 1.

5. TIGREAMS: TIGRO1131; ATP-Synt Gor A; 1.

6. TIGRO1131; ATP-Synt Gor A; 1.
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Statikovskaya E.B., Sukernik R.I., Derbeneva O.A., Volodko N.V.,
Statikovskaya E.B.,
Torroni A., Ruiz-Pesini E., Brown M.D., Lott M.T., Hosseini S.H.,
Huoponen K., Wallace D.C.,
"Mitochondrial DNA Diversity in Indigenous Populations of Southern
"Mitochondrial DNA Diversity in Indigenous Populations of Southern
Extent of Siberia, and the Origins of Native American Haplogroups.",
Ann. Hum. Genet. 0:0-0(2004).
-!- FUNCTION: Key component of the proton channel, it may play a
direct role in the translocation of protons across the membrane
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                        Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%; Score 42; DB 2; Length 226; 90.0%; Pred. No. 14;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JTD-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, ATP synthase F0 subunit 6.
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                Homo sapiens (Human).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human). Mitochondrion.
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SEQUENCE FROM N.A.
PubMed=14760490;
                                                                                                                              NCBI TaxID=9606;
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Name=ATP6;
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QGRKX7
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                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Landrace; TISSUE=Heart;
STRAIN=19363306; Pubmed=10433971;
MADLINE=193653306; Pubmed=10433971;
Lin C.S., Sun Y.L., Liu C.Y., Yang P.C., Chang L.C., Cheng I.C.,
Mao S.J.T., Huang M.C.;
"Complete nucleotide sequence of pig (Sus scrofa) mitochondrial genome and dating evolutionary divergence within artiodactyla.";
Gene 236:107-114(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogasawara N.; "Pig mitochondrial DNA: polymorphism, restriction map orientation, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H(+) (Out).
-!- SUBUNT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
-!- SUBCELDULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE OF 1-37 FROM N.A.
MEDLINE-86295557; PubMed=3017295;
Watanabe T., Hayashi Y., Kimura J., Yasuda Y., Saitou N., Tomita T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence data.";
Biochem. Genet. 24:385-396(1986).
-!- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                      Ursing B.M., Arnason U.; "The complete mitochondrial DNA sequence of the pig (Sus scrofa)."; J. Mol. Evol. 47:302-306(1998).
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EMBL; AF034253; AAD31190.1; -.
EMBL; M26139; AAD32031.1; -.
EMBL; T10977; T10977
InterPro; IPR000568; ATPsynt Asub.
Fram; PR00113; ATP-Synt A; 1.
PRINTS; PR00123; ATP-Synt Cor A; 1.
PR051179; PS00449; ATPASEA.

CCR(0); Hydrogen ion transport; Mitochondrion; Transmembrane.
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%; Score 42; DB 1; Length 226; 90.0%; Pred. No. 14; tive 0; Mismatches 1; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP synthase F0 subunit 6.
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                   SEQUENCE FROM N.A.
MEDLINE=98404150; PubMed=9732457;
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Matches 9; Conservative
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05-JUL-2004 (
05-JUL-2004 (
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RESULT 6

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Gaps

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2 NENLFASFIA 11
                1 NGNLFASFIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OGRLUB
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QERLUB
                                                                                 RESULT 9
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core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), peta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c (By similarity).

-i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-i- SIMILARITY: Belongs to the ATPase A chain family.

REMBL, AY495323; AR595301.i-.

REMBL, AY495323; AR595301.i-.

REMILARITY: Belongs to the ATPase A chain family.

REMBL, AY495133; ARF9571.i-.

REMILARITY: Belongs to the ATPase A chain family.

REMILARITY: Belongs to the ATPASE A chain family.

REMILARITY: PRO0129; ATPASEA.

INTERPAMS; TICRO1131; ATP_synt A: 1.

REMILARITY: PRO0129; ATPASEA.

INTERPAMS; TICRO1131; ATP_synt 6 or A; 1.

REMILARITY: PRO0129; ATPASE A; UNKNOWN 1.

REMILARITY: PRO0129; ATPASE A; UNKNOWN 1.

REMILARITY: PRO0120; ATPASE A; UNKNOWN 1.

REMILARITY: PRO0120; ATPASE A; UNKNOWN 1.

REMILARITY: PROGENIE ITANSPORT: ION TRANSPORT; Mitochondrion;

WA TRANSMEMBLANDS; TRANSPORT:

SEQUENCE 226 AA; 24783 MW; 578BEB0432E140FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=14760490;
Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Irwin J.A., Parsons T.J.;
Irwin J.A., Parsons T.J.;
Single nucleotide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:-0(2004).

-!-FUNCTION: Key component of the proton channel; it may play a
direct role in the translocation of protons across the membrane
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-:- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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Transmembrane; Transport.
SEQUENCE 226 AA; 24797 WW; 578FFF1436F550FA CRC64;
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                                                                                                                                                                                                               70.0%; Score 42; DB 2; Length 226; 90.0%; Pred. No. 14; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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PROSITE; PS00449; ATPASE A; 1.
                                                                                                                                                                                                                                                                                                                                                                                           Created)
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
ATP synthase F0 subunit 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                               Local Similarity 90.0
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Mitochondrion.
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-I CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP + phosphate + H(+)(Out).

-I SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha (3), peam (1), delta(1), epsilon(1).

-I SUBCELULIAR LOCATION: Integral membrane protein (By similarity).

-I SIMILARITY: Belongs to ATPase A chain family.

EMBL; AY495295; AAR95166.1; -.

EMBL; AY495295; Camicochondrion; IEA.

InterPro; IPR000568; ATPSPHT Asub.

PFam; PF00119; ATP-SYML A; 1.
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Coble M.D. Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J.; 
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Wararyota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 226 AA; 24775 MW; B5BC1EE8DBF54F0E CRC64;
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Last annotation update)
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Last annotation update)
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TIGRPAMS, TIGR01131, ATP_SYNt_6_or_Ā; l.
PROSITE; PS00449, ATPASE_Ā; l.
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PRT;
                                US-JUL-2004 (TrEMBLrel. 27, C. 05-JUL-2004 (TrEMBLrel. 27, Le 05-JUL-2004 (TrEMBLrel. 27, Le ATP synthase FO subunit 6. Name-ATP6;
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PRELIMINARY;
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Gaps

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/ Match 70.0%; Score 42; DB 2; Length 226; Local Similarity 90.0%; Pred. No. 14; 19 Conservative 0; Mismatches 1; Indels

1 NGNLFASFIA 10

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Transmembrane; Transport. SEQUENCE 226 AA; 24787 MW; 68B6236430292207 CRC64;

SEQUENCE Query Match

Best Loca Matches

GO, GO:0005739; C:mitochondrion; IEA.
InterPro; IPR000568; ATPSynt Asub.
Pfam; PF00119; ATP-synt A: 1.
PRINTS; PR00123; ATPASEA.
TIGRRAMS; TIGRO1131; ATP synt 6 or A; 1.
PROSTIE; P500449; ATPASEA; UNKNOWN 1.
CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;

Fri Nov 12 14:55:18 2004

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Gaps

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RESULT 11

H(+) (OUT).

-1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunites: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c (By similarity).

-1- SUBURELELULAR LOCATION: Integral membrane protein (By similarity).

-1- SIMILARITY: Belongs to the ATPase A chain family. Coble M.D., Just R.S., O'Callaghan J.B., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J., Island J.B., Deterson C.T., Island and Clearled polyworthisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians."; Int. J. Legal Med. 0:0-0(2004).

-i- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane (By similarity). -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606, 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATF synthase F0 subunit 6. 226 AA. PRT; Homo sapiens (Human). SEQUENCE FROM N.A. PubMed=14760490; Mitochondrion. Q6RMK9 Q6RMK9

ö Gaps Mitochondrion. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. ö CF(0); Hydrogen ion transport; Ion transport; Mitochondrion; 70.0%; Score 42; DB 2; Length 226; 90.0%; Pred. No. 14; tive 0; Mismatches 1; Indels DCB98F0136F5520F CRC64; 05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP synthase F0 subunit 6. PRINTS; PRO0123; ATPASEA. TIGREAMS; TIGR01131; ATP synt 6 or A; 1. PROSITE; PS00449; ATPASE A; 1. 24787 MW; Query Match Best Local Similarity 90.0 Matches 9; Conservative PRELIMINARY; Transmembrane; Transport SEQUENCE 226 AA; 2478 2 NENLFASFIA 11 1 NGNLFASFIA 10 Homo sapiens (Human). SEQUENCE FROM N.A. NCBI_TaxID=9606; QGRNG3; Q6RNG3 RESULT 12 Q6RNG3

2 NENLFASFIA 11

RESULT 13

Q6RNI4;

Q6RNI4

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H(+)(Out).

C -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c (By similarity).

C -!- SUBCELIULAR LOCATION: Integral membrane protein (By similarity).

C -!- SIMILARITY: Belongs to the ATPase A chain family.

RMBL; AX495199; ARR9318.1; --

DR GO; GO:0005739; C:mitochondrion; IEA.

CO; GO:0005739; C:mitochondrion; IEA.

DR FFEM; PRO0123; ATPSYRT Asub.

DR PRINTS; PR00123; ATPSYRT Asub.

TIGGRAMS; TIGRO1131; ATP SYNT 6.0r A; 1.

PROSITE; PS00449; ATPASEA.

TIGGRAMS; TIGRO1131; ATP SYNT 6.0r A; 1.
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PubMed=14760490;

Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

Irwin J.A., Parsons T.J.;

"Single nucleotide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.";

Int. J. Legal Med. 0:0-0(2004).

Int. J. Legal Med. 0:0-0(2004).

- FUNCTION: Key component of the proton channel; it may play a

direct role in the translocation of protons across the membrane
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-!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY:
increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
-!- FUNCTION: Key component of the proton channel; it may play a
direct role in the translocation of protons across the membrane
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-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
                                                                                              (By similarity).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Transmembrane; Transport.
SEQUENCE 226 AA; 24773 MW; 68B0ECAC0D655207 CRC64;
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Last annotation update)
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Pred. No. 14;
0; Mismatches
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Pfam: PF00119; ATP-SYNT_A; 1.
PRINTS; PR00123; ATPASEA.
TICREAMS; TICRO1131; ATP SYNT_6 or A; 1.
PROSITE; PS00449; ATPASE A; 1.
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Best Local Similarity 90..
Best Society 90..
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Q6RQ23
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Trubmed-14760490.

Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Truin J.A., Parsons T.J.;

Truin J.A., Parsons T.J.;

Increase the power of forensic testing in Caucasians.";

Increase that Just Increase have a components. (EV).

Increase the power of forensic increase a chain family.
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Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Irwin J.A., Parsons T.J.;
"Single nucleotide polymorphisms over the entire mtDNA genome that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                              Mitochondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Transmembrane; Transport.
SEQUENCE 226 AA; 24817 MW; 68B98F0136F55212 CRC64;
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Pred. No. 14;
0; Mismatches 1; Indels
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Last annotation update)
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Last annotation update)
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                             226 AA
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TIGREAMS, TIGR01131, ATP_SYNt_6_or_A; 1.
PROSITE, PS00449; ATPASE_A; 1.
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                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.08;
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Best Local Similarity 90..
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                             PRELIMINARY;
                                                                                                05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                                           ATP synthase F0 subunit
Name=ATP6;
                                                                     05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NGNLFASFIA 10
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Mitochondrion.
                                                                                                                                                                                          Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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CORRESPONT 14
CORRESPONT 16
CORRES

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Gaps

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1; Indels

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CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
Transmembrane; Transport.
SEQUENCE 226 AA; 24773 MW; 73B0FF12EDF79903 CRC64;
  S KW
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0; Gaps Query Match 70.0%; Score 42; DB 2; Length 226; Best Local Similarity 90.0%; Pred. No. 14; Matches 9; Conservative 0; Mismatches 1; Indels

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1 NGNLFASFIA 10 | | | | | | | | | | 2 NENLFASFIA 11

δλ g Search completed: November 10, 2004, 13:38:35 Job time : 15.6528 secs

27216, A 23740, A 5822, Ap 46698, A 370, App 26815, A 23, Appl 19574, A 24198, A

Sequence

36, Appl 51, Appl 5, Appli 7, Appli

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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US-09-252-991A-21163
US-09-252-991A-21163
Sequence 21163, Application US/09252991A
Sequence 21163, Application US/09252991A
Sequence 21163, Application US/09252991A
Sequence 21163, Application US/09252991A
Sequence 21163, Application Sequence 31.
Sequence 21163, Application US/09/252, 991A
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21163
LENGTH 196
TABLEST PLICATION NOS: 33142
SEQ ID NO 21163
LENGTH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.3%; Score 50; DB 4; Length 196; 45.0%; Pred. No. 11; 7; Indels iive 4; Mismatches 7; Indels
US-09-252-991A-27216
US-09-105-252-991A-27340
US-09-105-25A-5822
US-09-107-46698
US-09-108-452A-370
US-09-108-452A-370
US-09-108-452A-370
US-09-252-991A-19574
US-09-252-991A-2968
US-09-252-991A-2968
US-09-252-991A-2968
US-09-602-787A-296
US-09-602-787A-296
US-09-602-787A-296
US-09-257-591A-2968
US-09-257-591A-30379
US-09-252-991A-30379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TSPWTISSGLWPRLQKAAEA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSNWTSSAGAWSRTSGASTA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-21163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 45.0 Matches 9; Conservative
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5129, Ap Sequence 29866, A Sequence 12, Appl Sequence 28, Appl Sequence 1, Appli Sequence 7233, Ap Sequence 2, Appli Sequence 2, Appli Sequence 21765, A Sequence 21765, A Sequence 9, Appli Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21163, A
Sequence 18304, A
Sequence 20842, A
Sequence 2, Appli
Sequence 1, Appli
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17674, A
4, Appli
4, Appli
33, Appli
4, Appli
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31583, A
                                                                                     November 10, 2004, 12:32:37; Search time 10.0173 Seconds (without alignments) 191.991 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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Sequence
Sequence
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(GGDZ 6/ptodata1/iaa/5A_COMB.pep:*
/GGDZ 6/ptodata1/iaa/5B_COMB.pep:*
/GGDZ 6/ptodata1/iaa/6A_COMB.pep:*
/GGDZ 6/ptodata1/iaa/6B_COMB.pep:*
/GGDZ 6/ptodata1/iaaA/BCOMB.pep:*
/GGDZ 6/ptodata1/iaaA/PCTUS COMB.pep:*
/GGDZ 6/ptodata1/iaaA/PCTUS COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-21163
US-09-252-991A-21163
US-09-252-991A-20842
US-08-856-444-2
US-08-856-444-2
US-08-856-444-2
US-09-881-710-12
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-28
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-252-991A-25179
US-09-252-991A-25179
US-09-252-991A-25179
US-09-252-991A-25179
US-09-252-991A-25179
US-09-252-991A-25179
US-09-252-991A-25179
US-09-288-796A-17674
US-09-388-092-91
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                                                                                                                                                                  9
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                                                                                                                                        US-10-092-750-36
155
1 ILTSPWTTSSGLWPRLQKAAEAFKQLNQP
                                                                                                                                                                                                                                478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match
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                                                                                                                                                        Perfect score:
                                                                OM protein
                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                 Searched:
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| Patent No. 5747660
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
| TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
| NUMBER OF SEQUENCES: 51
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Fish & Richardson P.C. ADDRESSE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road, Suite 100
| CITY: Menlo Park STREET: US.A. STREET: California
| COUNTRY: US.A. STREET: CALIfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.3%; Score 48.5; DB 1; Length 879; Best Local Similarity 37.9%; Pred. No. 1.18+02; Matches 11; Conservative 3; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 343;
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MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC compatible
COMPUTER: Elem PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: NO. 5747660ember 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAB-TWOOD, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/POCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
31.3%; Score 48.5; D.
Best Local Similarity 52.6%; Pred. No. 36;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 LLTAPWSTRQG---RLQQA 245
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-698
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ILTSPWTTSSGLWPRLOKA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            879 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
; PUBLICATION INFORMATION:
US-08-856-444-2
                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-554-612C-1
                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
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US-08-554-612C-1
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US-09-252-291A-20842
Squence 20842, Application US/09252991A
Squence 20842, Application;
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUMBER: US/09/252,991A
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
SPICAR PAPLICATION NUMBER: US 60/074,788
SPICAR PAPLICATION NUMBER: US 60/094,190
SPICAR APPLICATION NUMBER: US 60/094,190
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                                                                            Score 49; DB 4; Length 462;
Pred. No. 44;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
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109 SSPWASASCCSRSGLMVRRSQPASCSIWPRLRKLA 143
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ZIP: 77071
COMPUTER TEADABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
RILING DATE: May 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
31.3%; Score 48.5; Di
Best Local Similarity 28.6%; Pred. No. 14;
Matches 10; Conservative 5; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20842
     , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18304
                                                                               Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                         ::||| ||: ||
24 ISSPWATSAAGWP 36
                                                                                                                                                                                     2 LTSPWTTSSGLWP 14
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GENERAL INFORMATION:
APPLICANT: DESPRES, Phillipe
APPLICANT: DESPRES, Phillipe
APPLICANT: COUTAGEOT, Marie-Pierre
APPLICANT: CATTEAU, Adeline
APPLICANT: CATTEAU, Adeline
FILE OF INVENTION: PRO-APOPTOFIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEINE
FILE REPERENCE: 2096/71US0
CURRENT APPLICATION NUMBER: US/09/881,710
CURRENT APPLICATION NUMBER: G/212,129
FRIOR APPLICATION NUMBER: G/212,129
FRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 39
TYPE: PRI CATUS
CORGANISM: Dengue virus
US-09-881-710-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DESPERS, Phillipe
APPLICANT: DEUBLE, Vincent
APPLICANT: CATTEAU, Adeline
TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEINE
FILE REFERENCE: 209671US0
CURRENT APPLICATION NUMBER: US/09/801,710
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DESPRES, Phillipe
APPLICANT: DESPRES, Vancer
APPLICANT: DEUBL, Vincer
APPLICANT: CATTEAU, Adeline
TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DEMGUE VIRUS ENVELOPE GLYCOPROTEIN:
FILE REPRENCE: 209671US0
CURRENT APPLICATION NUMBER: US/09/881,710
CURRENT APPLICATION NUMBER: US/09/881,710
PRIOR PILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 4;
Pred. No. 4.6;
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30.3%; Score 47; DB 4
Best Local Similarity 43.8%; Pred. No. 4.6;
Matches 7; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ed. No. 4.6;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Sequence 30, Application US/09881710 ; Patent No. 6673895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-881-710-28
; Sequence 28, Application US/09881710
; Patent No. 6673895
                                                                                                                                                                                                                                                                                                                                                                                                                                              30.3%; Sco-
43.8%; Pred
3; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Dengue virus
US-09-881-710-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-881-710-30
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                                                                                                                                                       Sequence 5129, Application US/09583110

Factor No. 6699703

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

CURRENT PRILING DATE: 109/09/583,110

CURRENT FILING DATE: 1090-05-26

FRIOR APPLICATION NUMBER: US 60/085,131

FRIOR FILING DATE: 1998-05-12

FRIOR FILING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29866, Application US/09252991A

Sequence 29866, Application US/09252991A

Sequence 29866, Application US/09252991A

Sequence 29866, Application US/09252991A

Sequence 20866, Application US/09252991A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 361;
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30.6%; Score 47.5; D
Best Local Similarity 50.0%; Pred. No. 55;
Matches 11; Conservative 2; Mismatches
                                                        248 VVSEWITEQGSWQEIQEKAVEVATVVIQP 276
            2 LISPWIISSGLWPRLQ-KAAEAFKQLNQP 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WITSSGLWPRLOKAAE-AFKQL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 WPTRPGSWPFQGKAAKRAFTQI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-583-110-5129
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; Sequence 12, Application US/09881710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29866
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US-09-252-991A-29866
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US-09-583-110-5129
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LENGTH: 361
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RESULT 13
US-09-252-91A-20461

US-09-252-91A-20461

Squence 20461, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: ARECULATION:
TITLE OF INVENTION: ARECULAND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARECULAND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARECULAND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARECULAND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20461

LENGTH: 146
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                                               LOCATION: 68

COTHER INFORMATION: Xaa=Asp or Glu
FEATURE:
NAME/KEY: UNSURE
LOCATION: 69

LOCATION: 69

COTHER INFORMATION: Xaa=Ala or Asp or His or Asn or Pro or Ser or Thr or US-09-513-999C-7233
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Patent No. 6482646

BRERAL INFORMATION:
GNERAL INFORMATION:
GNERAL TITLE OF INVENTION:
PILLE OF INVENTION: Plant Proteins that Interact with Nuclear Matrix
TITLE OF INVENTION: Proteins and Function as Transcriptional Activators
FILE REFERENCE: CL-13.1

CURRENT APPLICATION NUMBER: US/09/187,999A

CURRENT FILING DATE: 199-11-06

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                               Length 84;
                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                               Query Match 30.3%; Score 47; DB 4; Best Local Similarity 35.3%; Pred. No. 11; Matches 6; Mismatches 5
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US-09-187-999-2
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20461
                                                                                                                                                                                                                                                                                                                                                    13 WPRLQKAAEAFKQLNQP 29
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TYPE: PRT
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US-09-187-999-2
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US-09-881-710-1
US-09-881-710-1
US-09-881-710-1
Sequence 1, Application US/09881710
Sequence 1, Application US/09881710
Sequence 1, Application US/09881710
Sequence 1, Application US-0881710
GENERAL INFORMATION
APPLICANT: COURAGEOT, Marie-Pierre
APPLICANT: DEUBEL, Vincent
APPLICANT: DEUBEL, Vincent
APPLICANT: DEUBEL, Vincent
TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPROTEIN
FILLE REFERENCE: 2006-7100
CURRENT APPLICATION NUMBER: US/09/881,710
CURRENT FILING DATE: 2001-06-18
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 1
LENGTH: 76
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; Sequence 7233, Application US/09513999C
; Patent No. 6783961
; APPLICANT: Dumas Mine Edwards, J.B.
; APPLICANT: Dumas Mine Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TTLLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; Patent No. 6783961
; FILE REPERENCE: 59,USZ.REG
; CURRENT FILING DATE: 12000-02-24
; PRIOR PPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 7233
; LENGTH: 84
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                                                                                                                                                                                                                                                                                                                         3; Mismatches
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/212,129
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                           3 TSPWTTSSGLWPRLOK 18
                                                                                                                                                                                                                                                                                                                                                                                                        16 TETWMSSEGAWKQIQK 31
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52 TETWMSSEGAWKQIQK 67
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                                                                                                                                                                                                                                                                          Query Match 30.3
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                        TYPE: PRT GORGANISM: Dengue virus US-09-881-710-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT

CRGANISM: Dengue virus

US-09-881-710-1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-513-999C-7233
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RESULT 15

US-09-252-991A-25179

i Sequence 25179, Application US/09252991A

i Patent No. 6551795

i GENERAL INFORMATION:

i APPLICANTY MARCA J. Rubenfield et al.

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

ITILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

ITILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

ITILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25179

LENGTH: 210

TYPE: PRT

CORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.3%; Score 47; DB 4; Length 210; Best Local Similarity 39.3%; Pred. No. 34; Matches 11; Conservative 2; Mismatches 7; Indels
5 PWTTSSGLWPRLOKAAEA 22
                                 21 PMTTSFSIWPPTQRTRDA 38
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> 3 TSPWTTSSGLWPR-----LQKAAEA 22 : ||| | | | : || 16 SGPWTRRSGSWIRAGRCAVTPLQPSCEA 43

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Fri Nov 12 14:55:18 2004
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Sequence 1110, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
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US-10-296-115-1110
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Sequence 40845, A
Sequence 193474,
Sequence 233344,
Sequence 241808,
Sequence 241808,
Sequence 241808,
Sequence 1179, Ap
Sequence 31025,
Sequence 31255,
Sequence 31255,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Appl
                                                                      November 10, 2004, 16:36:12; Search time 31.1537 Seconds (without alignments) 328.807 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                1566620
GenCore version 5.1,6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-296-115-1110
US-10-767-701-4045
US-10-437-963-193444
US-10-437-963-193442
US-10-369-493-8143
US-10-104-047-2549
US-10-408-765A-1179
US-10-408-765A-1179
US-10-408-765A-1179
US-10-108-260A-3910
US-09-775-803-12
                                                                                                                          US-10-092-750-36
155
1 ILTSPWTTSSGLWPRLQKAAEAFKQLNQP 29
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                               1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Perfect score:
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Maximum DB seq
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Sequence 63, Appl
Sequence 344373,
Sequence 24426,
Sequence 257631,
Sequence 167190,
Sequence 27, Appl
Sequence 27, Appl
Sequence 227, Appl
Sequence 19217,
Sequence 192804,
Sequence 192804,
Sequence 192804,
Sequence 192804,
Sequence 192804,
Sequence 12, Appl
Sequence 12, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 20, Appl
Sequence 20, Appl
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US-10-092-750-36

// Sequence 36, Application US/10092750

// Sequence 36, Application US/10092750

// Publication No. US20030032157A1

// Publication No. US20030032157A1

// APPLICANT: Hammond, Philip W.

// APPLICANT: Alpin, Ualia

// APPLICANT: Alpin, Martin C.

// TITLE OF INVENTION: Polypeptides Interactive with BCL-X1

// TITLE OF INVENTION: Polypeptides US.10/092,750

// CURRENT APPLICATION NUMBER: US.002-03-07

// PRIOR APPLICATION NUMBER: US.002-03-07

// PRIOR PILING DATE: 2001-008

// WUMBER OF SEQ ID NOS: 253

// SEQ ID NOS: 8 SESEQ for Windows Version 4.0

// LENGTH: 29
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100.0%; Pred. No. 3.1e-14;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-092-750-36
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Length 600; Indels

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; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_89609C.1.pep

US-10-437-963-193474
                                                                                                                                                                                                                                           Query Match
35.5%; Score 55; DB
Best Local Similarity 58.8%; Pred. No. 52;
Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 192472, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 WIASALLWPRLAAALBSDERLGR 430
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  CURRENT FILING DATE: 2003-05-14 WINDERS OF SEQ ID NOS: 204966 SEQ ID NO 193474 LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                           429 WVVSARLWPRLADAIEA 445
                                                                                                                                                                                                                                                                                                                                               6 WITSSGLWPRLOKAAEA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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US-10-437-963-192472
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APPLICANT: LA ROSSA, Thomas J.
APPLICANT: LA ROSSA, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A,
APPLICANT: Boukharov, Andrey A,
APPLICANT: Broukharov, Andrey A,
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
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Publication No. US20040172684A1

Publication No. US20040172684A1

Publication No. US20040172684A1

APPLICANT: APPLICANT: Cao, Yonda

APPLICANT: Cao, Yonda

APPLICANT: Cao, Yonda

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REPERENCE: 38-21 [53535] B

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 40845

LENGTH: 259
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APPLICANT: Hyseq Inc
TILE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11.18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1110
LENGTH: 335
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Pred. No. 0.99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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US-10-767-701-40845
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 193474, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 14; Conservative 0
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-296-115-1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-437-963-193474
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US-10-767-701-40845
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APPLICANT: LA ROSA: Thomas J.
APPLICANT: LA ROSA: Thomas J.
APPLICANT: La Rosa: David K.
APPLICANT: La Rosa: Julia
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 192472
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Sequence 233344, Application US/10425115
Sequence 233344, Application No. US20040214272A1
SEQUENCE 233344, Application No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Labou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Shou, Yihua
APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_88698C.1.pep
US-10-437-963-192472
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Gaps

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APPLICANT: The standy sing the stands and stands are stands and stands and stands are stands and stands are st
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32.9%; Score 51; DB 16; Length 2131;
Best Local Similarity 36.0%; Pred. No. 6.8e+02;
Matches 9; Conservative 6; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%; Score 51; DB 14; Length 793; 36.0%; Pred. No. 2.5e+02; ive 6; Mismatches 10; Indels
       Score 51; DB 17; Length 175;
Pred. No. 52; 7; Indels
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION AND TO THE SEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392Ale1 full length cDNA
FILE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR FILING DATE: 2002-03-25
PRIOR FILING DATE: NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 2549
LENGTH: 793
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                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-10-104-047-2549
; Sequence 2549, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
                   Query Match
Best Local Similarity 29.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 36.0°
--hes 9, Conservative
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CRGANISM: Homo sapiens
US-10-104-047-2549
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; Sequence 8143, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Galer, Steven C.
APPLICANT: Galer, Steven C.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EARRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8143
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; Sequence 24.808, Application US/10425115
; Sequence 24.808, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION;
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: About Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 24.808
; MUMBER PLANTS
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 24.808
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Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 4; Mismatches 8; Indels
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US-10-425-115-241808
                                                   ; OTHER INFORMATION: Clone ID: NRT4577_144402C.1.pep
US-10-425-115-233344
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                             5 PWITSSGL--WPRLOKAA 20
                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Thermobifida fusca
US-10-369-493-8143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
ORGANISM: Zea mays
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US-10-369-493-8143
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LENGTH: 566
TYPE: PRT
CRGANISM: Mus musculus
US-09-775-803-12
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RESULT 11
US-10-425-115-301225
US-10-425-115-301225
Sequence 301225, Application US/10425115
Sequence 301225, Application No. US20040214272A1
Sequence 301225, Application No. US2004214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Vinua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
CURRENT RILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 301225
LENGTH: 108
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Publication No. US20030167487A1
GENERAL INFORMATION:
APPLICANT: COR Therapeutics, Inc.
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Ramakrishnan, Vanitha
TITLE OF INVENTION: Transgenic Animals Having a Modified Glycoprotein V
TITLE OF INVENTION: Gene and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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| Publication No. US20040005560A1
| GENERAL INFORMATION:
| APPLICANT: HELIX RESEARCH INSTITUTE
| TILL OF INVENTION: No. US20040005560A1e1 full length cDNA
| FILE REFRENCE: H1-A0106
| CURRENT APPLICATION NUMBER: US/10/108,260A
| CURRENT FILING DATE: 2002-03-27
| NUMBER OF SEQ ID NOS: 5458
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 3 Patentin Ver. 2.1
| SEQ ID NO 3 Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: MRT4577_37793C.1.pep
US-10-425-115-301225
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OTHER INFORMATION: unsure at all Xaa locations
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / ORGANISM: Homo sapiens
US-10-108-260A-3910
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
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US-10-108-260A-3910
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APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Schaderna, Steven K
APPLICANT: Zerhusen, Bryan D
TITLE OF INVENTION: Proteins, Polynuclectides Encoding Them and Methods of TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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CURRENT APPLICATION NUMBER: US/09/775,803
CURRENT FILING DATE: 2001-02-05
PRIOR PEPLICATION NUMBER: PCT/US99/17594
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US/10/080,334
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,523
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/322,712
PRIOR PLILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-13
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-604
PRIOR FILING DATE: 2001-03-604
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/21,521
PRIOR APPLICATION NUMBER: 60/31,525
PRIOR APPLICATION NUMBER: 60/311,595
PRIOR APPLICATION NUMBER: 60/311,595
PRIOR APPLICATION NUMBER: 60/210,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 228, Application US/10080334
Publication No. US20040002584A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gangolli, Esha A
Padigaru, Muralidhara
Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spytek, Kimberly A
Vernet, Corine A. M.
Malyankar, Uriel M
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pena, Carol E. A. APPLICANT: Shimkets, Richard A APPLICANT: Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Furtak, Katarzyna
Tchernev, Velizar T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gusev, Vladimir Y
Casman, Stacie J
Boldog, Ferenc L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 NPWLCDCGLWPFLQ 434
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Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SPWITSSGLWPRLQ 17
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Best Local Similarity 57.1
Matches 8; Conservative
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Pred. No. 2.4e+02;
1; Mismatches 5; Indels
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Miller, Charles E
APPLICANT: Fisen, Andrew J
TILLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/274,295
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/218,526
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-02-17
PRIOR PILING DATE: 2001-02-17
PRIOR PILING DATE: 2001-02-17
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-03-16
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A PAPLICATION NUMBER: 60/260,018
DR FILING DATE: 2001-01-05
DR APPLICATION NUMBER: 60/260,360
DR FILING DATE: 2001-01-08
R FILING DATE: 2001-01-08
DR APPLICATION NUMBER: 60/272,411
DR FILING DATE: 2001-02-28
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VS-10-03-417-105
VS-10-03-417-105
Sequence 105, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
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Malyankar, Uriel M
Rothenberg, Mark
Stone, David J
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Edinger, Shlomit R
Sciore, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boldog, Ferenc L
Guo, Xiaojia
Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-080-334-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SPWTTSSGLWPRLO 17
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| PRIOR FILING DATE: 2001-03-02
| PRIOR APPLICATION NUMBER: 60/291,186
| PRIOR PILING DATE: 2001-065-15
| PRIOR PELING DATE: 2001-07-05
| PRIOR PELING DATE: 2001-07-05
| PRIOR PELING DATE: 2001-07-02
| PRIOR PELING DATE: 2001-07-12
| PRIOR PAPLICATION NUMBER: 60/318,405
| PRIOR PELING DATE: 2001-09-12
| PRIOR PAPLICATION NUMBER: 60/318,700
| PRIOR PELING DATE: 2001-09-12
| PRIOR PELING DATE: 201-09-12
| PRIOR PELING DATE: 20
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GenCore version 5.1.6
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using sw model protein search, OM protein Run on:

November 10, 2004, 12:29:32; Search time 6.46114 Seconds (without alignments) 431.857 Million cell updates/sec

Title: Perfect score:

US-10-092-750-36 155 1 ILTSPWTTSSGLWPRLQKAAEAFKQLNQP 29

Scoring table: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		S	two-component sens	ethylbil	probable enzyme Z2	probable enzyme [i	biotin biosynthesi	probable periplasm	egg membrane prote	thetical	hypothetical prote	aminopeptidase (le	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	phosphoprotein pho	hypothetical prote	polyprotein(C, E,	genome polyprotein	genome polyprotein	genome polyprotein	eps8 protein - mou	epidermal growth f	겁	hypothetical prote	probable transcrip	o)	cal	hypothetical prote
SULPHANIS	Ę	- 1	T36983	AI2255	IBEG	œ	F90894	B64906	AI0163	ın	H71535	T49721	F90602	T37923	D95106	G83536	H81690	S41854	T49265	A47311	C32401	B32401	A32401	539983	I38728	GNWVWP	59	8298	221	T51548	
	c g	3	N	N	Н	~	N	(1	N	0	~	N	0	N	N	N	Ŋ	Ñ	N	N	N	N	N	ď	N	Н	Ŋ	N	N	α	N
	Length	5	282	401	480	252	252	252	378	424	698	831	454	688	361	450	253	281	441	775	792	792	792	821	822	1226	~	305	466	599	103
d	% Query Match		ď	ď	ď.	31.6	÷.	4	Ξ.	Ξ.	Ξ.	4	ä	ä	ö	ö	ö	ö	30.3	ö	ö	ö	ö	ö	ö	ö	ö		。	。	ę.
	9	3 :	.50	20	20	49	49	49	49	49	49	49	48	48	47.5	47.5	47	47	47	47	47	47	47	47	47	47	47	٠	46.5	•	46
	Result	2	н	7	M.	4	Ŋ	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

32.3%; Score 50; DB 2; Length 401; 40.9%; Pred. No. 23;

Query Match Best Local Similarity

hypothetical prote probable V-ATPase,	probable glucarate probable glucarate	probable exonuclea hypothetical prote	hypothetical prote	glucarate denydrat	probable acyl-CoA	hypothetical prote	glucoamylase (imbo	Clp ATPase [import	membrane alanyl am	glycine cleavage s	B1 protein - black	protein A - flock
F84716 T47216	H91084 A85930	AG2363 F72089	F86534	H65060	D96805	F98136	AE3151	AH0437	A53984	AG2381	QQBBB1	S41397
0 0	77	0 0	N	N	N	N	N	~	7	~	н	0
169	340 365	413	419	446	691	775	800	867	963	983	966	998
29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7	29.7
4 4 6	4 4 6 4	4 4	46	46	46	46		46	46	46	46	. 46
30	3 3 3 3	. W. W.	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 T36983
	product transposars surepromycs C.Species: Greptomyces coelicolor C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
	CiAccession: T3698; No. 1 Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999 A.Reference number: Z21618
	A;Accession: 130393; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Mosidues: 1.282 - COLIS A;Cross-references: UNIPROT:O9R192; EMBL:AL109949; PIDN:CAB52897.1; GSPDB:GN00070; SCOEDE A;Experimental source: strain A3(2)
	C;Seneils:SCUII.12 A;Gene: SCOEDB:SCUII.12 C;Superfamily: Streptomyces coelicolor probable transposase SC6G9.36c
	Query Match Best Local Similarity 53.3%; Pred. No. 16; Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
	Oy 3 TSPWITSSGLWPRLQ 17
	RESULT 2
-	A12255 two-congrount sensor histidine kinase all3600 [imported] - Nostoc sp. (strain PCC 7120)
	Cipate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
	C;Accession: AI2255 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
	DNA Res. 8. 205-213, 2001 A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A,Reference number: AB1807, MUID:21595285, PMID:11759840
	A,Accession: A12255 A,Status: preliminary A,Molecule type: DNA
	A, Residues: 1-401 <kur> A;Cross references: UNIPROT:Q8YR50; GB:BA000019; PIDN:BAB75299.1; PID:g17132733; GSPDB:GP A;Experimental source: strain PCC 7120</kur>
	C,Genetios: A,Gene: all3600 C,Superfamily: sensory transduction system regulatory protein homolog

7 TTSSGLWPRLQKAAEAFKQLNQ 28

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Conservative

9;

Matches

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R;HHYABSH, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. Mah, Res. B, 11-22, 2001
A;Hills: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; WUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: B64906
C;Accession: B64906
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1.252 «HAY»
A;Cross-references: UNIPROT:Q8XAZ2; GB:BA000007; PIDN:BAB35549.1; PID:g13361592; GSPDB:GN
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P76145; GB:AE000249; GB:U00096; NID:g1787790; PIDN:AAC74592.1
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: bioC protein; bioC homology
F;32-130/Domain: bioC homology <BIOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R. Parkhill, J.; Wren, B. W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; f. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F. Mature 413, 523-527, 2001
Agticle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUD:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable periplasmic binding protein YPO1343 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
                                                                                                                           - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
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                                                                                                                                                                    C,Species: Escherichia coli
C,Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C,Accession: F90894
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C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biotin biosynthesis protein homolog b1519 - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A,Residues: 1-252 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%; Score 49; DB
llarity 47.6%; Pred. No. 19;
Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: BCs2126
C,Superfamily: bioC protein; bioC homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 WVTATGLRPWLQDLTESEQQL 216
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                                                                                                                               probable enzyme [imported]
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les 10; Conserv
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                    Nydroxymethylbilane synthase (EC 4.3.1.8) precursor - Buglena gracilis
Nydroxymethylbilane synthase (EC 4.3.1.8) precursor - Buglena gracilis
Nydroxymethylbilanes: porphobilinogen deaminase; pre-uroporphyrinogen synthase
C;Becies: Buglena gracilis
C;Cacession: S06109
R;Sharif, A.L.; Smith, A.G.; Abell, C.
Bur. J. Blochem. 184, 353-359, 1989
A;Title: Isolation and characterisation of a cDNA clone for a chlorophyll synthesis enzy
A;Reference number: S06109; MuID:90005485; PMID:2477247
A;Accession: S06109
A;Accession: S06109
A;Accession: S06109
A;Accession: S06109
A;Residues: 1-480 <SHA>
A;Cross-references: UNIPROT:P13446; GB:X15743; NID:g18411; PIDN:CAA33759.1; PID:g18412
A;Accession: Soft this sequence, including the amino end of the mature protein, was confired by the con
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossidues: 1-252 <STO>
A;Cross-references: UNIPROT:Q8XAZ2; GB:AE005174; NID:g12515147; PIDN:AAG56247.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
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K;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description: catalyzes the stepwise polymerization of four molecules of porphobilinoge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Pathway: porphyrin biosynthesis
A;Note: acting with uroporphyrinogen-III synthase (cosynthase), which cyclizes hydroxyme C;Superfamily: hydroxymethylbilane synthase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; chlorophyll biosynthesis; chloroplast; F;1-139/Domain: transit peptide (chloroplast) #status predicted <INP>
F;140-480/Product: hydroxymethylbilane synthase #status experimental <MAT>
F;395/Modified site: dipyrrolylmethanemethyl (Cys) (covalent) #status predicted
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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Gaps
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Mismatches
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5 PWTTSSGLWPRLQKAAEA 22

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A, Gene: Z2186 C, Superfamily: bioC protein; bioC homology

C;Genetics:

Query Match Best Local Similarity Matches 10; Conserv

Best Loca Matches

WITSSGLWPRLQKAAEAFKQL 26

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A;Accession: T37933
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Nolecule type: DNA
A;Rosidues: 1-688 <CON>
A;Cross-references: UNIPROT:Q10109; EMBL:Z68198; PIDN:CAA92388.1; GSPDB:GN00066; SPDB:SP?
A;Experimental source: strain 972h-; cosmid c18G6
C;Genetics:
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                                                       CiSpecies: Neurospora crassa
CiDate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
CiDate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
CiAccession 149721
Submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Reference number: 225022
A;Reference number: 225022
A;Amolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-831 cSCH>
A;Cross-references: UNIPROT: 09P5J5; EMBL:AL356172; GSPDB:GN00116; NCSP:B23L21.340
A;Experimental source: BAC clone B23L21; strain OR74A
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hypothetical protein B21121.340 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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31.6%; Score 49; DB 2; Length 831;
Best Local Similarity 38.1%; Pred. No. 73;
Matches 8; Conservative 5; Mismatches 8; Indels
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6; Mismatches
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Pred. No.
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A,Gene: MYDU 7260
A,Genetic code: SGC3
C,Superfamily: Cytosol aminopeptidase
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Best Local Similarity 36.8%;
Matches 7; Conservative 6
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <KUR>
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A;Gene: NCSP:B23L21.340
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C;Species: Chlamydia trachomatis
R;Stephens, R:S; Kalman, S:; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
C;Stephens, R:S; Kalman, S:; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
A;Aincession: H71535
A;Accession: H71535
                                                  A;Molecule type: DNA
A;Residues: 1-378 <KUR>
A;Cross-references: UNIPROT:Q8ZGF8; GB:ALS90842; PIDN:CAC90172.1; PID:g1S979391; GSPDB:G
C;Genetics:
A;Gene: YP01343
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A, Residues: 1-424 <CHA-
A, Cresidues: 1-424 <CHA-
A, Cresidues: 1-424 < CHA-
A, Cresidues: 1-6424 < CHA-
C, Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology
F;110-364/Domain: ZP domain homology < ZPH->
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C;Species: Cyprinus carpio (common carp)
C;Species: Cyprinus carpio (common carp)
C;Date: 09-Unn-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52847
B;Chang, Y:, Wang, S.; Tsao, C.; Huang, F.
submitted to the EMBL Data Library, April 1995
A;Description: Structural analysis and expression of carp ZP3 gene.
A;Reference number: S52847
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                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 2; Length 378 Pred. No. 30;
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31.6%; Score 49; DB
Best Local Similarity 39.1%; Pred. No. 30;
Matches 9; Conservative 2; Mismatches
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Best Local Similarity 33.3'
Matches 10; Conservative
                         A;Status: preliminary
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δ g RESULT 10 T49721

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A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Fesidues: 1-253 <TET>
A.Cross-references: UNIPROT:Q9PKB1; GB:AE002323; GB:AE002160; NID:g7190585; PIDN:AAF39395
A.Experimental source: strain Nigg (MoPn)
A.Genetics:
A.Genetics:
                                                                                                                                                               conserved hypothetical protein frameshift TC0556 [imported] - Chlamydia muridarum (strair
                                                                                                                                                                                                                                                                                                                   RiRead, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
Affilies Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                              Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SPWITSSGLW----PRLOKAAEAFKQLNQP 29
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30.3%;
Best Local Similarity 33.3%;
Matches 10; Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Streptococcus protein SP0921 [imported] - Streptococcus pneumoniae (strain TIGR Cispecies: Streptococcus pneumoniae
Cjaceis: Streptococcus pneumoniae
Cjaceis: Streptococcus pneumoniae
Cjaceis: Streptococcus pneumoniae
Cjaceis: Osawa 2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
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44.4%; Pred. No. 60;
                                                                                                                                                         Length 688;
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A;Gene: SP0921
C;Superfamily: uncharacterized conserved protein SP0921
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                                                                                                                                                    31.0%; Score 48; DB 2; llarity 50.0%; Pred. No. 82; Conservative 2; Mismatches
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llarity 50.0%; Pred. No. 47;
Conservative 2; Mismatches
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Best Local Similarity
A,Gene: SPDB:SPAC18G6.10
A,Map position: 1
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4

Gaps 4 ;

Length 253; Indels

Score 47; DB 2; Pred. No. 37;

7; Mismatches

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996689 homo sapien
998730 mus musculu
998730 mus musculu
998730 mus masculu
662ub3 homo sapien
672bm7 desulfovibr
662ub3 homo sapien
82086313 homo sapien
82086313 homo sapien
8213212 bacillus an
8413212 bacillus an
8413212 bacillus
891428 oryza sativ
970758 synechococc
88978 encephalito
9881 pseudomonas
98981 pseudomonas
99396 callitrichi
661b9 gibberella
661b9 gibberella
821019 gibberella
821019 gibberella
821019 gibberella
821019 streptomyce
88426 homo sapien
9708542 homo sapien
9708542 homo sapien
9708546 euglena gra
98133 oryza sativ
908730 rattus nory
994203 mus musculu
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                                                                                                       2004, 12:27:34 ; Search time 35.4111 Seconds (without alignments) 471.205 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                   1825181
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 ILTSPWTTSSGLWPRLQKAAEAFKQLNQP 29
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                                                                                                                                                                                                                                                                                                              1825181 segs, 575374646 residues
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0291KX9
02946KX3
02946KX3
02728M7
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067724
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071DZ9
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Q9R192
Q8YR50
Q8YYA8
HEM3 EUGGR
Q8LJA3
GPV RAT
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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Q9wt88 tt virus. o Q7sad6 neurospora Q6ix33 hypholoma f Aat37495 hypholoma Q27072 teamia soli Q76925 neurospora Q6xi13 drosophila Q6xj13 drosophila Aar10040 drosophila Aar06869 drosophila Q9w3w8 drosophila Q7pux3 anopheles g Q8xaz2 escherichia P76145 escherichia	te) tae; Buteleostomi; ths old; c.R., Schuler G.D., c.F., Bhat N.K., M., Hong L., t.T.L., Scheetz T.E., no.P., Prange C., no.P., Mullahy S.W., Globs R.A., igues S., Sanchez A., Bouffard G.G., on M.C., M., Butterfield Y.S., rch A., Schein J.E., rch A., Schein J.E.,	databases. F CRC64; Length 400; Indels 0; Gaps 0;
2 Q9WT88 2 Q7GAD6 2 Q7GAD6 2 QAT37495 2 QAT37495 2 QAT37495 2 QAT35 2 QAT315 2 QAT315 2 QAT318 2 QAT318 2 QAT318 1 TAM_ECO57 1 TAM_ECO57	PRT; 400 AA. Treated) Last sequence update Last sequence update Last sequence update Last sequence update Sciurognathi; Muri; Sciurognathi; Muri Nagner L., Shenmen Wagner L., Shenmen Wagner L., Shenmen Wagner L., Shenmen Letow K.H., Schaefer Wagner L., Shenmen Letow K.H., Schaefer Magner L., Abanen Letow K.H., Schaefer Magner L., Shenmen Letow K.H., Schaefer Letow R.H., Maker Losavan Loshiyuki S., Carni Peters G.J., Abramso Hele S., Garcia A.M., Ac., Shevchenko Y., Abramso Garcia B.J., Lu X. M., Madan M., Rodr. Garcia D.J., Myers Schmutz J., Myers Schmutz J., Myers Schmutz J., Myers Schmutz J., Myers Smailus D.E., Schne yeis of more than 15	alpha model. 7 mor IBL/GenBank/DDBJ de id. E50B9205El39ECEF icore 67; DB 2; I Pred. No. 0.66; Mismatches 0;
32.3 31.9 31.9 31.9 31.9 31.9 31.6 31.6 31.6 31.6 31.6 31.6 31.6 31.6	11 1 177 1891VT7 1	SEQUENCE FROM N.A. SIRALN=mix FVB/N; SIRALN=mix FVB/N; SISUB-Mammary tumor. WAP-TGF Strausberg R.; Submitted (JUN-2001) to the EX EMBL; BC009098; AAH09098.1; MGD; MGI-2138828; Eps812. INEAFPC; IPR011036; PH relate InterPrc; IPR011036; PH relate InterPrc; IPR011036; PH PID. PROSITE; E01179; PID; 1. SEQUENCE 400 AA; 44839 MW; ery Match set Local Similarity 100.0%; sttches 14; Conservative 0;
66886668884444444444444444444444444444	RESULT 1 C091VT7 D0 C091VT7 D1 C0	ក៏ស័ន្

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RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;

RX Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

RX Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

RA Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Hischul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Diatchenko L., Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

RA Diatchenko L., Warusina K., Farmer A.A.; Rubin G.M.; Hong L.;

RA Diatchenko L., Warusina K., Farmer A.A.; Rubin G.M.; Hong L.;

RA Diatchenko L., Warusina K., Farmer A.A.; Rubin G.M.; Hong L.;

RA Diatchenko L., Woldin T.B.; Toenlyowis S., Carninof P., Frange C.,

RA Raha S.S.; Loquellano N.A.; Peecers G.J.; Abramson R.D.; Mullahy S.J.;

RA Richards S., Worley K.C.; Hale S., Garcia A.M.; Gay L.J.; Hulyk S.M.;

RA Hilalon D.K.; Mizny D.W.; Sodergren B.J.; Lu X.; Gibbs R.A.;

Rahey J., Helton E., Ketteman M.; Madan A.; Gibbs R.A.;

Rhiting M., Madan A.; Young A.C.; Shevchenko Y.; Boulfard G.G.;

Ry Hiting M., Madan A.; Young A.C.; Schwechenko Y.; Boulfard G.G.;

Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;

Ry Timpon and initial analysis of more than 15,000 full-length human and wave and wones constant and sevenes and analysis of more than 15,000 full-length human
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Submitted (MAR.2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005492; AAH05492.1; -..
HSSP; Q08509; InC.
MGD; MGI:2138828; Eps812.
MGD; MGI:2138828; Eps812.
InterPro; IPR01036; Preceptor activity; IEA.
InterPro; IPR01036; Praelated.
InterPro; IPR006020; PTB_PID.
InterPro; IPR001831; 11.
ProDom; PP000166; SH3 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00018; SH3 1; 1.
ProDom; PD000066; SH3; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01179; PID; 1.
PROSITE; PS50002; SH3; 1.
Receptor; SH3 domain.
SEQUENCE 729 AA; 82229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Q9H6S3
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MEDILNE=22508195; PubMed=12620401;

MIDLINE=22508195; PubMed=12620401;

Trochetti A., Confalonieri S., Scita G., Di Fiore P.P., Betsholtz C.;

Trochetti A., Confalonieri S., Scita G., Di Fiore P.P., Betsholtz C.;

Trochetti A., Confalonieri S., Scita G., Di Fiore P.P., Betsholtz C.;

Trochetti A., Confalonieri S., Scita G., Di Fiore P.P., Betsholtz C.;

Trochetti A.C. Season Drofile, and protein structure.";

Genomics 81:234-244(2003).

R MESL; AAC74929; AAL7618.1; -.

R MESL; AAC74929; AAL7618.1; -.

R MESP; Q08509; IICC.

GO; GO:0004872; Freceptor activity; IEA.

R InterPro; IPRO1036; PH related.

R InterPro; IPRO10452; SH3.

R InterPro; IPRO10452; SH3.

R ProDom; PD000066; SH3. 1.

R PROSITE; PS01179; PID; 1.

R PROSITE; PS01179; PID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Watanabe K., Kumagal A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Epidermal growth factor receptor pathway substrate 8-like protein
                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein FLJ22171 (Epidermal growth factor receptor pathway substrate 8 related protein 2).
Name=EPSSR2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.2%; Score 67; DB 2;
100.0%; Pred. No. 1.2;
ative 0; Mismatches (
                                                                                                                                                                                            715 AA
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                                                                        275 RLOKAAEAFKOLNO 288
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                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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SEQUENCE FROM N.A.
STRAIN=Mix FVB/N;
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Best Local Similarity
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SEQUENCE
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Q99K30;
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оэнекэ;
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Matches
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Q99K30
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AK025589; BAB15180.1; -.
Genew; HGNC:21296; EPS8L2.
                                                                                                                 Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                       Length 729;
                                                                                                              0; Indels
82229 MW; A11DE82FF2C0BD18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Q9H6S3 PRELIMINARY; PRT; 743 AA. O9H6S3; CONTROL TEMBLED. 16, Created) 01-MAR-2001 (TrEMBLed. 16, Last sequence update) 01-OCT-2003 (TrEMBLed. 25, Last annotation update) Hypothetical protein FLJ21935.
                                                 Query Match
43.2%; Score 67; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 14; Conservative 0; Mismatches
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NCBI_TaxID=9606;
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AAS96086;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA ligase, NAD-dependent (EC 6.5.1.2).
Name=ligA, OrderedLocusNames=DVU1608;
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 2; Length 743;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                743 AA; 83792 MW; DB01D8F6363A1F80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q72BM7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OGO, GO: 0003911; F:DNA ligase (NAD+) activity; IEA. GO; GO: 0016874; F:ligase activity; IEA. GO; GO: 0016874; F:ligase activity; IEA. InterPro; IFR001679; BNALigase.
InterPro; IFR001679; DNALigase.
InterPro; IFR000445; HhH.
InterPro; IFR008994; Nuoleic acid OB.
InterPro; IFR008994; Nuoleic acid OB.
InterPro; IFR010994; RuyA_2_like.
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                                                                                                                                                                                                                                                                                                                                                                                                 ch 43.2%; Score 67; DB 1 Similarity 100.0%; Pred. No. 1.2 14; Conservative 0; Mismatches
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InterPro; IPR004149; Znf_DNAligase_C4.
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Pfam; PF03120; DNA_ligase_OB; 1.
Pfam; PF03119; DNA_ligase_ZBD; 1.
Pfam; PF00633; HHH; 1.
InterPro; IPR011036; PH related.
InterPro; IPR006020; PTB_PID.
InterPro; IPR00145; SH3_F1D.
Fām; PF00018; SH3_1; 1.
ProDom; PD000066; SH3; 1.
SMART; SM0326; SH3; 1.
PROSITE; PS01179; PID; 1.
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                                                                                                                                                                                                                                                                                                  SH3 domain.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-2004 (TrEMBLrel. 27, Created)
27-APR-2004 (TrEMBLrel. 27, Last sequence update)
11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
10-MA ligase, NAD-dependent (EC 6.5.1.2).
11-MA Ligase, NAD dependent (EC 6.5.1.2).
11-MA Ligase, NAD dependent (EC 6.5.1.2).
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65-JUL-2004 (TrEMBLrel. 27, Last sequence update)
65-JUL-2004 (TrEMBLrel. 27, Last annotation update)
65-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ43854.
Hypothetical protein FLJ43854.
Hypothetical protein FLJ43854.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelecstomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  o;
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                                                                                               SMART; SM00532; LIGANC; 1.

TICRFAMS; TIGR00575; dalj; 1.

PROSITE; PS50172; BRCT; 1.

PROSITE; PS101056; DNA_LIGASE_N2; 1.

COMplete proteome; DNA_repair; DNA_replication; Ligase; NAD.

SEQUENCE 799 AA; 86098 NW; 535A6009B6B60EA3 CRC64;
                                                                                                                                                                                                                                                                                                                           'Match 36.1%; Score 56; DB 2; Length 799; Local Similarity 62.5%; Pred. No. 48; es 10; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.1%; Score 56; DB 2; Length 799; 62.5%; Pred. No. 48; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               799 AA; 86098 MW; 535A6009B6B60EA3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|||| ||| ||:
270 TAPWTTHSGLMARLRE 285
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ProDom; PD003944; DNAligase;
SMART; SM00292; BRCT; 1.
SMART; SM00278; HhH1; 3.
SMART; SM00532; LIGANC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TSPWTTSSGLWPRLOK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TSPWITSSGLWPRLQK 18
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les 10; Conservative
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Hypothetical protein (Fragment).
Name=PY07765;
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NON TER
SEQUENCE
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                     Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T., A. Ota T., Nakagawa S., Senoh A., Mizuguchi H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Xamashita H., Matsuo K., Nakamura Y., Sekine M., Kimura K., Magatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Sugano S., Nagahari K., Submitted (JUL-2003) to the EWBL/GenBank/DDBJ databases.

EMBL, AKI2542; ARG86313.1;
EMBL, AKI2542; ARG86313.1;
EMBL, AKI2542; ARG86313.1;
EMBL, AKI2542; ARG86313.1;
EMBL, AKI2542; ARG8631.1;
EMBL, AKI2542; ARS8631.1;
EMBL, AKI2542; ARS8631.1;
EMBL, AKI2542; ARS8631.1;
EMBL, AKI2542; ARS8631.1;
EMBL, SES0341; DENN, 1.
EFam; PF0315; PRR.
EFam; PF0315; PRR.
EFam; PR051TE; PS50941; DENN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Yawai-Hio Y., Saito K., Nishikawa T., Kimuza K., Yamashita H., Mateuo K., Nakamuza Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Muzakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AK125642; BAC86313.1.
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                    4.
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                                                                                                                                                                                                                                                                                         Length 1557;
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Joseph 1557;
Local Similarity 36.4%; Pred. No. 1.38+02;
les 12; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                      35.5%; Score 55; DB 2; Le ilarity 36.4%; Pred. No. 1.3e+02; Conservative 5; Mismatches 12;
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513 VLESPWPSSTRSGIFLWTKVRNVVRGLAQFRQP 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ILTSPW--TTSSG--LWPRLQKAAEAFKQLNQP 29
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1557 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          707 A.A.
                                                                                                                                                                                                                                                                                                                                               1 ILTSPW--TTSSG--LWPRLQKAAEAFKQLNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA FLJ43854 fis, clone TESTI4007064.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                  Local Similarity
ses 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC86313
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Q7R724;
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Matches
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SENGMENCE FROM N.A.

SENGMENCE FROM N.A.

STRAINE-Amed / isolate Porton,

Read T.D., Peterson S.N., Toursase N.J., Baillie L.W., Paulsen I.T.,

Read T.D., Peterson S.N., Toursase N.J., Baillie L.W., Paulsen I.T.,

Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hann P.C., Kolstoe A.-B., Fraser C.M.;

The genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii,";
Nature 419:512-519/2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary date.
EMBL, AABLO1002913; EAA20293.1; -.
                                                                                                                                                                                                                                                 Garlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Chackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Salzberg S.L., Venter J.C., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
pasmodium yoelii yoelii.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.8%; Score 54; DB 2; Length 707; 50.0%; Pred. No. 82; ive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          707 707
707 AA; 77054 MW; DC40A56BA854AEFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBINGO, CEHUD4; OGKUM1, 01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2004 (TrEMBLrel. 24, Last annotation update) Prophage LambdaBa02, Clp protease family protein. OrderedLocusNames=BA4092, BAS3804; ORFNames=GBAA4092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 VLAWPWTLPPSVWRRLQLAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ILTSPWTTSSGLWPRLQKAA 20
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STRAIN=Ames / isolate 0581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Nature 423:81-86(2003)
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                                                                                                                                                         SEQUENCE FROM N.A.
                                                                            NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                              PubMed=12368865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1392;
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Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Mimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Antonio B.A., Kanamori H., Antonio M., Hayashi M., Ando T., Aoki H., Arita K., Hamada M., Hardad C., Hajishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Rarasawa W., Katagiri S., Kikuta A., Kobayashi M., Kono I., Antonia K., Machara T., Mixuno H., Mizubayashi T., Nukai Y., Nadamiti N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M., Animokawa T., Shomura A., Song T., Takazaki Y., Terasawa K., Tauji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Imama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Yama M., Jiang J., Gojobori T., Khan J.H., Kim H.I., Eun M.Y., Tetrasaki W., Nature 420,312-316(2002).
      Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0699D11 (Similar to Arabidopsis thaliana chromosome 1 YAC VUP8H12R sequence).
                                      uryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22225697; PubMed=12917641; DOI=10.1038/nature01943; Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L., Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J., Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.; The genome of a motile marine Synechococcus."; An uniterbury J.; Nature 424:1037-1042(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.9%; Score 52.5; DB 2; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.2%; Score 53; DB 2; Length 460; ilarity 43.5%; Pred. No. 73; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 AA; 28619 MW; B874CA4D098CA7D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02458; Transferase; 1.
SEQUENCE 460 AA; 48759 MW; 33BA11150391880B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BX565692; CAE07643.1; -.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR000620; DUF6.
Pfan; PF00892; DUF6; I.
Complete proteome; Hypothetical protein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003480; Transferase.
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OrderedLocusNames=SYNW1128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP002817; BAB03452.1; -. EMBL; AP001366; BAA92409.1; -. EMBL; AP001366; BAA92405.1; -.
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hes 10; Conserv
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                                                                                                                                                                                                SEQUENCE FROM N.A.
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0
Federova N.B.,
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B. Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M. "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017334; AAT33212.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                           ., Hill K.,
Okinaka R.
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Fed
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.2%; Score 53; DB 2; Length 251; 35.7%; Pred. No. 39; sive 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.2%; Score 53; DB 2; Length 251; 35.7%; Pred. No. 39;
                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus anthracis str. Ames 0581.
Bacillus, firmicutes, Bacillales, Bacillus, Bacillus cereus group; Bacillus anthracis.
NCBI_TaxID=261594;
                                                         "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AA; 28154 MW; 373E72DE6082EE71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 AA; 28154 MW; 373E72DE6082EE71 CRC64;
                                                                                                                                                                                                                                                                                                                   GO; GO:0008462; F:endopeptidase Clp activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPRO1907; Pept_S14 ClpP.
Pfam; PF00574; CLP protease; I.
PRINTS; PR00127; CLPPROTEASEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
Prophage LambdaBa02, Clp protease family protein.
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ILTSPWTTSSGLWPRLQXAAEAFKQLNQ 28
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01-JUN-2004 (TrEMBLrel. 27, Last seq
01-JUN-2004 (TrEMBLrel. 27, Last ann
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
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Best Local Similarity 35....
Conservative
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                     SEQUENCE FROM N.A.
                     Wilson M., S
Fraser C.M.,
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Q9LDZ9
ID Q9LDZ9
AC Q9LDZ9
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AAT33212
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Search completed: November 10, 2004, 13:38:37 Job time : 37.4111 secs
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SETRALIN=DCISON
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
Madupu R., Daugherty S.C., Brinkac L.M., Beanam M.J., Haft D.H.,
Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Encephalitozoon cuniculi.
Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
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01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
11-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
11-MAR-2004 (TrEMBLrel. 26, Last family.
12-MAR-2004 (TremBlater, LysR family.
13-MAR-2004 (Pv. Lomato).
13-MAR-2004 (Pv. Lomato).
13-MAR-2004 (Pv. Lomato).
13-MAR-2004 (Pv. Lomato).
14-MAR-2004 (Pv. Lomato).
15-MAR-2004 (Pv. Lomato).
16-MAR-2004 (Pv. Lomato).
17-MAR-2004 (Pv. Lomato).
18-MAR-2004 (Pv. Lomato).
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                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR008994; Nucleic_acid_OB.
Hypothetical protein.
SEQUENCE 413 AA; 47285 MW; FOA401A6DDBFFF89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein BCU05_1050.
Name=ECU05_1050;
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Best Local Similarity 50.0%; Pred. No. 51; Matches 11; Conservative 2; Mismatches
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                                                                                                                                                      6 WITSSGLWPRLOKAAEAFKQLN 27
                                                                                                                                                                                                                                                       16 WTTASGMWRSLSDQGSAL-QLN 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=GB-M1;
MEDLINE=21576510; PubMed=11719806;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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Q8SVI8
ID Q8SVI
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Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
Belaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
Bender C.L., White O., Fraser C.M., Collmer A.;
I'The complete genome sequence of the Arabidopsis and tomato pathogen
I'The complete genome sequence of the Arabidopsis and tomato pathogen
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I'The Complete genome sequence of the Arabidopsis and tomato pathogen
I'The Complete genome sequence of the Arabidopsis of Go. 10003100; Firtanscription factor activity; IEA.

INTERPORT IPROMOSSIS; HTH Lyse.
INTERPORT IPROMOSSIS; HTH Lyse Subst.
InterPro; IPROMOSSIS; Wing—Interpor; IPROMOSSIS; Ming—Interpor; IPROMOSSIS; 
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Complete protecme, DNA-binding, Transcription regulation.
SEQUENCE 306 AA, 34681 MW, BE98F966404F962F CRC64,
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Pred. No. 78;
7; Mismatches
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Best Local Similarity 36.4
Matches 12; Conservative
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Sequence 26717, A Sequence 32786, A Sequence 48003, A Sequence 22121, A Sequence 5973, Ap Sequence 12472, A Sequence 5, Appli
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Sequence 5, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 33963, A
Sequence 49180, A
Sequence 21, Appl
Sequence 21, Appli
Sequence 21, Appli
Sequence 2, Appli
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Sequence 3, Appl:
                                                                      November 10, 2004, 12:32:37; Search time 11.0535 Seconds (without alignments) 191.991 Million cell updates/sec
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(GGTZ 6/ptodata1/laa/5B_COMB.pep:*

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(GGTZ 6/ptodata1/laa/PCTUS COMB.pep:*

(GGTZ 6/ptodata1/laa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-270-767-32786
US-09-270-767-32786
US-09-252-991A-22121
US-09-252-991A-22121
US-09-253-991A-31679
US-09-253-991A-31679
US-09-543-611A-5973
US-09-568-102-5
US-09-568-102-5
US-09-568-486-5
US-09-03-03-1186
US-09-03-03-1186
US-09-003-03-2
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1 RTLQPRLLQNQQQHLPALPIWFLLQWLRLHPL 32
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US-08-535-837-3
US-09-620-405B-471
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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471,		13909		17, Appl	17,	516,	516,	516,	516,	516,	516, App	4860	23315, A	4230, Ap	44204, A	
Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	
US-09-433-826B-471 US-09-604-287A-471	US-09-834-759-471	US-US-590-751A-471 118-09-489-0398-13909	US-08-694-865-17	US-09-124-491-17	US-09-383-912-17	US-09-082-279B-516	US-09-315-304B-516	US-09-834-784-516	US-09-515-965A-516	US-09-350-641C-516	US-09-350-841A-516	US-09-621-976-4860	US-09-252-991A-23315	US-09-134-000C-4230	US-09-270-767-44204	ALIGNMENTS
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154 154	154	154 721	1403	1403	1403	39	39	39	33	39	8	94	181	183	354	
27.8	27.8	8.7.6	27.8	27.8	27.8	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	
4 4 0 0	4 ·	4, 4	4, 4,	49	4	4 8	48	48	48	48	48	4,	48	48	48	
7 5 8 7 8	30	31	1 M	34	32	36	37	38	39	40	41	42	43	44	45	

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GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
GURRENT PRILING DATE: 1999-02-12
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR FILING DATE: 1998-08-13
FRIOR FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) LOCATION: (87); OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknow US-09-248-796A-26717
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| Sequence 32786, Application US/09270767
| Patent No. 6703491
| GENERAL INFORMATION: GENERAL INFORMATION: All APPLICANT: Homburger et al. TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster: FILE REFERENCE: File Reference: 7326-094
| CURRENT APPLICATION NUMBER: US/09/270,767
| CURRENT FILING DATE: 1998-03-17
| NUMBER OF SEQ ID NOS: 62517
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 32786
| LENGTH: 312
| TYPE: PRT
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47.6%; Pred. No. 0.77;
tive 5; Mismatches 6; Indels
5.09-248-796A-26717
Sequence 26717, Application US/09248796A
Patent No. 6747137
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Best Local Similarity 47.6
Matches 10; Conservative
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Sequence 471, App

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RESULT 6
US-09-252-991A-31679
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Patent No. 6521795

GENERAL INFORMATION:
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABACUSTOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE OF INVENTION: ABACUSTOSA FOR DIAGNOSTICS AND THERAPEUTICS
TURBENT TILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PAPILOM NUMBER: US 60/094,190

PRIOR PELING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22121

TYPE: PRT

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Sequence 48003, Application US/09270767
Sequence 48003, Application US/09270767
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48003
LENGTH: 312
                                                                                                                                                                                                     Gaps
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                                                                                                                     DB 4; Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LOPRILQNOQOHLPA----LPIWFLLQWLRLHP 31
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Pred. No. 2.9;
1; Mismatches
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Pred. No. 9.9;
1; Mismatches
                                                                                                                                                                                                     1; Mismatches
                                                                                                            Query Match 32.4%; Score 57;
Best Local Similarity 54.2%; Pred. No. 2
Matches 13; Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                       185 OPTLILNTIOHWPALHKWLDINYL 208
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US-09-543-681A-5973
; Sequence 5973, Application US/09543681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 OPRLLONQOQHLPALPIWFLLQWL 27
; ORGANISM: Drosophila melanogaster
US-09-270-767-32786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), ORGANISM: Drosophila melanogaster
US-09-270-767-48003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.4%;
Best Local Similarity 54.2%;
Matches 13; Conservative :
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Best Local Similarity 48.5%;
Matches 16; Conservative
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILJ
TITLE OF INVENTION: UCCLEIC AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILLING DATE: 12000-04-05
PRIOR FILLING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INPORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE:
107196-1136
CURRENT APPLICATION NUMBER:
US 60/074,768
PRIOR PILING DATE:
1999-02-18
PRIOR PILING DATE:
1999-02-18
PRIOR FILING DATE:
1999-07-27
NUMBER OF SEQ ID NOS:
33142
LENGTH:
199
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Patent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
CURRENT FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12472
LENGTH: 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.1%; Score 53; DB 4;
Best Local Similarity 37.5%; Pred. No. 14;
Matches 12; Conservative 6; Mismatches E
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5973
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5973
LENGTH: 398
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US-09-568-480-5

Sequence 5, Application US/09568480

Patent No. 6355458

GENERAL INFORVATION:

APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Application General

APPLICANT: Goarlach, Joern

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 1000-05-10

CURRENT FILING DATE: 1000-05-10

PRIOR APPLICATION NUMBER: 09/35,409

PRIOR APPLICATION NUMBER: 09/35,409

PRIOR PELING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PATENTIN Ver: 2.0

SEQ ID NO SEG ID NOS: 30
                                                                                                                                                                                                    RESULT 10
US-09-567-969-5

Sequence 5, Application US/09567969

Batent No. 635547

GENERAL INFORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Molnar, Istvan

APPLICANT: Molnar, Istvan

APPLICANT: Gerlach, Joern

APPLICANT: Gerlach, Joern

APPLICANT: Gerlach, Joern

TILLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFRENCE: 4-3052A

CURRENT APPLICATION NUMBER: US/09/567,969

CURRENT PILING DATE: 2000-05-10

PRIOR APPLICATION NUMBER: 09/335,409

PRIOR PILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH 1257
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                                                                                   |: ||: || || || || 4499 TVDARLIVVRQPAGLTPAQAATVPVAFLTAWLALHDL 4534
                              2 TLOPRILONQOOHL-PA----LPIWFLLOWLRIHPL 32
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// ORGANISM: Sorangium cellulosum
US-09-568-480-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.7%;
Matches 15; Conservative
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Sequence 5, Application US/09568102

Patent No. 6346404

GENERAL INFORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Molnar, Istvan

APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Goerlach, Joern

TILL OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT APPLICATION NUMBER: US/09/568,102

CURRENT APPLICATION NUMBER: 09/335,409

PRIOR FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 7257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09335409
| Patent No. 6121029
| General Information
| APPLICANT: Schupp, Thomas
| APPLICANT: Schupp, Thomas
| APPLICANT: Ligon, James
| APPLICANT: Ligon, James
| APPLICANT: Zirkle, Ross
| APPLICANT: Cyr, Devon
| APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels 5;
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                                                                                                                                               DB 4; Length 301;
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29.3%; Score 51.5; DB 3;
Best Local Similarity 41.7%; Pred. No. 6.2e+02;
Matches 15; Conservative 4; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                     6 RLLONQOOHLPALPIWFLLOWL-----RLH 30
                                                                                                                                            Query Match 29.3%; Score 51.5; D
Best Local Similarity 43.8%; Pred. No. 17;
Matches 14; Conservative 2; Mismatches
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Sorangium cellulosum US-09-568-102-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Sorangium cellulosum
US-09-335-409-5
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US-09-335-409-5
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Gaps

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Score 51.5; DB 3; Length 7257; Pred. No. 6.2e+02; 4; Mismatches 12; Indels 5
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SENERAL INFORMATION:
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US-09-270-767-33963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                Sequence 3. Application US/09568486

Patent No. 6355459

GENERAL INFORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Gerlach, Joern

TILLE OF INVENITON: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-3052A

CURRENT FILING DATE: 2000-05-10

PRIOR PILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 5

LENGTH: 7257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09568472

Patent No. 6358719

GENERAL INFORMATION:

APPLICANT: Chupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Cyr, Devon

APPLICANT: Cyr, Devon

APPLICANT: General Joern

TILLE REFERENCE: 4-30582A

CURRENT FILING DATE: 2000-05-10

PRIOR PLICATION NUMBER: 09/335,409

PRIOR FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SEGTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT CRGANISM: Sorangium cellulosum US-09-568-486-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Sorangium cellulosum
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RESULT 14 US-09-567-899-5 ; Sequence 5, Application US/09567899 ; Patent No. 6383787

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Patent No. 6703491

GRNERAL INFORMATION:
APPLICANT: Homburer et al.
TITLE OF INVENTION: Valeic acids and proteins of Drosophila melanogaster TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33963
LENGTH: 135
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: All Stvan
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr Devon
APPLICANT: Lose
APPLICANT: Cyr Devon
APPLICANT: Jose
APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) TYPE: PRT

) ORGANISM: Sorangium cellulosum

US-09-567-899-5
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Best Local Similarity 41.7%;
Matches 15; Conservative
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 527
LENGTH: 7257
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Sequence 27,1834, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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US-10-092-750-37
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Matches 32
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Sequence 21834,
Sequence 106, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 71590, A
Sequence 17590, A
Sequence 17590, A
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449, App
12, Appl
                                                                                                                                                      November 10, 2004, 16:36:12; Search time 34.3765 Seconds (without alignments) 328.807 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PcT_Rew PUB.Pepp:*

2: /cgn2_6/ptodata/1/pubpaa/PcT_Rew PUB.Pepp:*

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5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USIOM_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-425-115-271834
US-10-037-417-106
US-10-220-475A-4
US-10-419-629-4
US-10-072-012-448
US-10-696-699A-4
US-10-425-117-1590
US-10-220-475A-17
US-10-220-475A-2
US-10-072-012-451
US-10-072-012-49
US-10-072-012-49
US-10-072-012-49
US-10-072-012-49
US-10-072-012-49
US-10-073-012-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1566620 seqs, 353225886 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 105, App Sequence 279796, Sequence 314612, App Sequence 18, Appl Sequence 18, Appl Sequence 1877, App Sequence 78, Appl Sequence 73, Appl Sequence 118557, Sequence 10228, Appl Sequence 240589, Sequence 240589, Sequence 240589,	Sequence 270451, Sequence 2026, Ap Sequence 1672, Ap Sequence 270450, Sequence 240781, Sequence 80, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl
5 US-10-037-417-105 5 US-10-44-599-279796 108-10-425-115-362182 108-10-425-115-362182 108-10-425-115-324612 108-10-300-846-18 108-10-300-445-18 108-10-300-445-18 108-10-47-91-34 108-10-47-91-34 108-10-47-91-34 108-10-48-10-38	5 US-10-422 4 US-10-011 5 US-10-422 7 US-10-422 10S-09-771 US-09-901 0 US-09-901 3 US-10-014
242 404 404 404 404 404 404 404	225 236 236 236 236 236 236 24 25 25 26 26 26 26 26 26 26 26 26 26 26 26 26
56. 56. 56. 56. 56. 56. 56. 56. 56. 56.	
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ALIGNMENTS

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100.0%; Pred. No. 2.8e-15;
iive 0; Mismatches 0;
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CRGANISM: Homo sapiens
US-10-092-750-37
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-417-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-10-220-475A-4
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant and Construct and C
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR APPLICATION NUMBER: 60/303,231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_179504C.1.pep
US-10-425-115-271834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.2%; Score 65.5; DB 17; Best Local Similarity 48.4%; Pred. No. 4; Matches 15; Conservative 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 EQQQPHQPQLP-WFLQRQRPPVLLPWLRPHP 398
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Publication No. US20040052806A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson, David W
Padigaru, Muralidhara
Taupier Jr, Raymond J
Miller, Charles E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burgess, Catherine E
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gorman, Linda
Edinger, Shlomit R
Sciore, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ellerman, Karen
Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patturajan, Meera
Grosse, William M
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rothenberg, Mark
Stone, David J
Boldog, Ferenc L
Guo, Xiaojia
Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays
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APPLICANT:
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PRIOR PLINGO NETE: 2010-10-05

PRIOR PLINGO NETE: 2010-07-12

PRIOR PLINGO NETE: 2010-07-12

PRIOR PLINGO NETE: 2010-09-10

PRIOR PLINGO NETE: 2010-09-10
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, , Gaps

10;

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Sequence 71590, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Avoil, David K.
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Parameter Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules Thereof for Plant Improvement
FILING DATE: 2003-04-28

UURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

MUMBER OF SEQ ID NOS: 73128

SEQ ID NO 71590

LENGTH: 71

LENGTH: 71

LENGTH: 71

LENGTH: 71
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APPLICANT: Kline, Kimberly
APPLICANT: Yu, Weiping
APPLICANT: Yu, Weiping
APPLICANT: Yu, Weiping
FILE APPLICANT: Liul, Hui
APPLICANT: Hantash, Feras
TITLE OF INVENTION: Tocopherol Associated Protein and Uses Thereof
FILE REFERENCE: D6453GIP
CURRENT APPLICATION NUMBER: US/10/696,699A
CURRENT FILING DATE: 2003-10-29
FRIOR FILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 4
TENGRAL APPLICATION NUMBER: US 10/419,629
SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.4%; Score 57; DB 16; Length 403; Best Local Similarity 44.4%; Pred. No. 46; Astches 16; Conservative 3; Mismatches 7; Indels 3
                                                                                                                                                                                    Score 57; DB 15; Length 403; Pred. No. 46; 7; Indels 13; Mismatches 7; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KREY: PEPTIDE
1 OTHER INDEMATION: TAP-46 polypeptide
US-10-696-699A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10696699A
Publication No. US20040152883A1
GENERAL INFORMATION:
                                                                                                                                                                                             Query Match
Best Local Similarity 44.4%;
Matches 16; Conservative
SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 448 LENGTH: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-448
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-114-71590
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NUMBER OF SEQ ID NOS: 1391
                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                              Query Match 32.4%; Score 57; DB 15; Length 403; Best Local Similarity 44.4%; Pred. No. 46; Matches 16; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCANT: Furtak, Katarzyna
CCANT: Grosse, William M.
CCANT: Grosse, William M.
CCANT: Lepley, Denise M.
CCANT: Rieger, Daniel K.
CCANT: Rieges, Catherine E.
S. OF INVENTION: Proteins and Nucleic Acids Encoding Same
REFERENCE: 21402-258
                                                                                                                                                                                                                                                                                                                                                                                          3 LOPR-----LLONQOCHLPALP---IWFLLOWLR 28
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CURRENT PELICATION NUMBER: US/10/072,012
CURRENT PILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR PRIOR DATE: 2001-01-31
PRIOR PRIOR DATE: 2001-01-31
PRIOR PILING DATE: 2001-02-02
PRIOR PRIOR DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PRIOR DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PRIOR DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PRIOR DATE: 2001-02-05
PRIOR PRIOR DATE: 2001-02-05
PRIOR PRIOR DATE: 2001-02-05
PRIOR PLING DATE: 2001-02-07
                                                                                                                                                                      NAME/KEY: PEPTIDE
) OTHER INFORMATION: TAP-46 polypeptide
US-10-419-629-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 448, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
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Gerlach, Valerie
Taupier Jr, Raymond J.
Gusey, Vladimir Y.
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Anderson, David W.
Rastelli, Luca
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Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colman, Steven D. Wolenc, Adam R. Pena, Carol E. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chernev, Velizar
     NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
                                                          LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                              FEATURE:
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Gaps

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Sequence 2. Application US/10220475A
Publication No. US20040023227A1
Publication No. US20040023227A1
GENERAL INPORMATION:
APPLICANT: INOUE, KEIZO
APPLICANT: ARITA, MAKOTO
FILE REFERENCE: 04853.0056-00000
CURRENT APPLICATION: DNA ENCODING SQUALENE EPOXIDASE-PROMOTING FACTOR
FILE REFERENCE: 04853.0056-00000
CURRENT FILING DATE: 2002-08-30
FRIOR FILING DATE: 2001-03-01
FRIOR FILING DATE: 2001-03-01
FRIOR FILING DATE: 2000-03-02
FRIOR FILING DATE: 2000-03-02
FRIOR FILING DATE: 2000-03-02
FRIOR FILING DATE: 2000-03-02
FRIOR PRICE SEQ ID NOWER: 2010-03-02
FRIOR PRICE SEQ ID NOW 2
FRIOR PLANCENT ON NUMBER: 2000-03-02
                   FILE REFERENCE: 21402-256

CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265,102

PRIOR APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31

PRIOR PELLOR DATE: 2001-01-31

PRIOR PELLOR OF TELLOR NUMBER: 60/265,517

PRIOR PELLOR DATE: 2001-01-31

PRIOR PELLOR DATE: 2001-01-01

PRIOR PELLOR DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266,406

PRIOR PELLOR DATE: 2001-02-05

PRIOR PELLOR DATE: 2001-02-05

PRIOR PELLOR DATE: 2001-02-07

PRIOR PELLOR DATE: 2001-02-07

PRIOR PELLOR DATE: 2001-02-07

PRIOR PELLOR DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR PELLOR DATE: 2001-02-07

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 403;
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local Similarity 56.5%; Pred. No. 53;
Matches 13; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 QNQQQHLPALP---IWFLLQWLR 28
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US-10-072-012-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-10-220-475A-2
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US-10-220-475A-17

Sequence 17, Application US/10220475A

Publication No. US20040023227A1

GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: ARAI, HIROYUC

APPLICANT: ARAI, MAKOTO

TITLE OF INVENTION: DNA ENCODING SQUALENE EPOXIDASE-PROMOTING FACTOR
FILE REFERENCE: 04653.0096-00000
CURRENT APPLICATION NUMBER: DCT/JP01/01592
FRICR APPLICATION NUMBER: DFT/JP01/01592
FRICR FILING DATE: 2002-03-01
FRICR FILING DATE: 2000-03-01
FRICR FILING DATE: 2000-03-02

PRICR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 17
                                                                                                         32.1%; Score 56.5; DB 15; Length 71; larity 32.5%; Pred. No. 9.9; Conservative 9; Mismatches 7; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17164H05_F11.pep
US-10-425-114-71590
                                                                                                                                                                                                                                                            4 OPRILONQOOHLPALPI-----WFLLOWL-----RLHPL 32
                                                                                                                                                                                                                                                                                                   Query Match 32.1%; Score 56.5; DB 15; Best Local Similarity 56.5%; Pred. No. 53; Matches 13; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 QNQQQHLPALP --- IWFLLQWLR 28
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Publication No. US20040033493A1
GENERAL INFORMATION:
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Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
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Taupier Jr, Raymond J.
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burgess, Catherine E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
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Brosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colman, Steven D.
Wolenc, Adam R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carol E. A
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Rieger, Daniel K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                    Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-220-475A-17
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                                                                                                            Query Match
                                                                                                                                                                                  Matches
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TYPE: PRT
ORGANISM: Mus musculus
US-09-775-803-12
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NT Raderson, bo.,
NT Raderson, bo.,
NT Raderson, bo.,
NT Ratelli, Luca

ANT Galach, Valerie

ANT Taupier Jr. Raymond J.

CANT Colman, Steven D.

CANT Colman, Steven D.

CANT Colman, Steven D.

CANT Gorses, William M.
LICANT Lepley Denie M.

PLICANT Lepley Denie M.

PLICANT Lepley Denie M.

PLICANT Lepley Denie W.

PLICANT PRIGGES. 1402-238

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THE REPRENE 2140-238

THE REPRENE 2001-01-31

PRICE PLING DATE: 2001-02-05

PRICE PL
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32.1%; Score 56.5; D
Best Local Similarity 56.5%; Pred. No. 53;
Matches 13; Conservative 3; Mismatches
Sequence 449, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
                                                                                         . Tchernev, Velizar
Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
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JOURNAL TO SEQUENCE 12, Application US/09775803

PUBLICATION NO. US20030167487A1

GENERAL INFORMATION:

APPLICANT: Remarktishnan, Vanitha

APPLICANT: Phillips, David

TITLE OF INVENTION: Transgenic Animals Having a Modified Glycoprotein V

TITLE OF INVENTION: Gene and Methods for Their Use

TITLE OF INVENTION: 124481-5044-US

CURRENT APPLICATION NUMBER: US/09/775,803

CURRENT FILING DATE: 1999-08-04

PRIOR FILING DATE: 1999-08-04

PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 12

LENGTH: 566
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier, Chr. Raymond J
APPLICANT: Taupier, Chr. Raymond J
APPLICANT: Taupier, Charles E
APPLICANT: Miller, Charles E
APPLICANT: Bisen, Andrew J
TILLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 2140-2235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR PRILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.1%; Score 56.5; DB 10; Length 5
Best Local Similarity 46.7%; Pred. No. 74;
Matches 14; Conservative 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 PQLTQVLLGHNPWLCDCGLWPFLQWLRHHP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PRILONOCOHLPAL---PIWFLLOWLRLHP 31
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Publication No. US20040052806A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiachong
APPLICANT: Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ellerman, Karen
Malyankar, Uriel M
Rothenberg, Mark
Stone, David J
Boldog, Perenc L
Guo, Xiaojia
Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, Li
Gorman, Linda
Edinger, Shlomit R
Sciore, Paul
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Indels

9 QNQQQHLPALP---IWFLLQWLR 28

ð 쉱 RESULT 13

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Sequence 27996, Application US/10424599

Sequence 27996, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: Rovalic David K

APPLICANT: Rovalic David K

APPLICANT: APPLICANT: Application Yihua

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICAND NOWES: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 279796

LENGTH: 90

TYPE: PRT

CORANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.1%; Score 56.5; DB 15; Length 567; Best Local Similarity 46.7%; Pred. No. 74; Matches 14; Conservative 2; Mismatches 11; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 31.8%; Score 56; DB 15; Length 90; Best Local Similarity 38.5%; Pred. No. 14; Matches 10; Conservative 7; Mismatches 9; Indels
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US-10-424-599-279796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(90)
FEATURE INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 POLTOVLLGHNPWLCDCGLWPFLOWLRHP 440
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17 MKPRIVSLKIEHLVXLPRWFXTQVLK 42
PRIOR FILING DATE: 2001-02-28

PRIOR PLING DATE: 2001-03-02

PRIOR PLING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/291,186

PRIOR PILING DATE: 2001-05-15

PRIOR PILING DATE: 2001-05-15

PRIOR PILING DATE: 2001-07-05

PRIOR PILING DATE: 2001-07-05

PRIOR PILING DATE: 2001-07-05

PRIOR PILING DATE: 2001-07-12

PRIOR PILING DATE: 2001-07-12

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2001-09-10

PRIOR PILING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 227

SOFTWARE: PACENTIN VET. 2.1

SEQ ID NO 105

LENGTH: 567

TYPE: PAT

CREANISM: MUS MUSCULUS

US-10-037-417-105
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US-10-424-599-279796
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Search completed: November 11, 2004, 01:28:19 Job time : 35.4265 secs

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5.1.6
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GenCore version
(c) 1993 - 2004
         Copyright
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OM protein - protein search, using sw model

Run on:

November 10, 2004, 12:29:32 ; Search time 7.12953 Seconds (without alignments) 431.857 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-092-750-37 176 1 RTLQPRLLQNQQQHLPALPIWFLLQWLRLHPL 32

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	hypothetical prote	_			rec	olfactory receptor	tocopherol associa	끍		ם	hypothetical prote		v	hypothetical prote	olfactory receptor		_	_	hypothetical prote	escapes X-inactiva	cation-transportin	hypothetical prote	OD:	beta-D-galactosida	ų	e:		prec	hypothetical prote
SUMMARIES	T33922	AC1896	F82493	T00333	H23701	S29707	JC7708	T31334	AB2475	B90558	T38996	T40985	A37286	E75219	S20571	AC3602	T36045	AE2167	T22139	I84689		D96502	GBEC	E90678	A85529	A23207	ZIZM23	B22831	AG1925
Length DB	!				314 2															,			024		024				303 2
% Query Match 1	38.1	34.1	31.2	31.2	30.4	0	0	6	6	6	29.5	φ.	ď.	6	29.0	φ.	φ.	29.0	σ.	В.	28.4	28.4	ω.	28.4	φ.	28.1	8	ω.	28.1
Score	67	9	55	55	53.5	E	53	52.5	~	52	52	51.5	~	51	51	51	51	51	51	20	20	20	20	20	20	49.5	9	σ	49.5
Result No.		~	m	4	ω	9	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

,	4	27	α	199	0	T27239	hypothetical prote
) r	1 7		a	216	۱,		olfactory receptor
7 0	n (0 0	9 6	١ (Christophia boto
32	4, .	7	2 0 (0 e	٧ (Cystachitonine Deta
33	49	27.8	00	203	7		propable snort-cha
34	49	27.	80	612	ď		probable long-chai
35	49	27.	00	830	~		prolactin receptor
36	48.5	27.	9	267	N		alpha kafirin - so
37	48.5	27.6	o	313	0		hypothetical prote
38	48.5	27.	بو	790	Ŋ		hypothetical prote
39	48	27.3	m	147	0		hypothetical prote
40	48	27.3	m	186	N	D83323	probable acetyltra
41	48	27.3	m	566	N		
42	48	27.	m	282	N		hypothetical prote
43	48	27.3	m	451	N		
44	47.5	27.0	0	515	N		
4.5	47.	27.0		5	n	,,	hypothetical prote
?		;	>)			
						ALIGNMENTS	
RESULT 1							
homotherical protein Y849A.2	ical pro	14010	484	0. A 0	ť,	- Caenorhabditis elegans	
C; Species: Caenorhabditis elegans	s: Caen	orhab	diti	s elec	yan	18	
C; Date:	29-0ct-	1999	#sed	nence	r.	C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change	ange 09-Jul-2004
C; Access	ion: T3.	3922				ı	
R; Courtn	ey, L.;	Lang	geton	Υ.;	ŭ	R;Courtney, L.; Langston, Y.; Drone, K.; Mead, K.	
submitte	d to the	e EME	3L Da	ta Lil	ora	submitted to the EMBL Data Library, February 1999	
A; Description: The sequence	ption:	The s	segue	nce of	n D	of C. elegans cosmid Y8A9A.	
A;Refere	nce num	ber:	2214	39			
A; Accession: T33922	ion: T3	3922					
A;Status	: preli	minar	٦ :	ransl	ate.	A;Status: preliminary; translated from GB/EMBL/DDBJ	
A; Molecule type: DNA	le type	. DNA	,				
A; Residues: 1-1360 < COU>	es: 1-1	360 •	COC				
A;Cross-	referen	ces:	TIND	ROT	ξi	A, Cross-references: UNIPROT: Q9TYK4; EMBL: AF125461; PIDN: AAD12852.1; GSFDB: GN00020;	12852.1; GSPDB:GN00020; CESP:)
A; Experimen	mental	sourc	 	traın	Br	A; Experimental source: strain Bristol NZ; clone Y8A9A	
1							

C;Genetics: A;Gene: CSSP:Y8A9A.2 A;Map position: 2 A;Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3; 848/2; 944/2; 1044/2; 10	Query Match 38.1%; Score 67; DB 2; Length 1360; Best Local Similarity 47.4%; Pred. No. 0.75; Matches 18; Conservative 3; Mismatches 9; Indels 8; Gaps 1;	3 LOPRILLONOQOHLPALPIWPILIQWIRLHPL 32
C,Genetics: A,Gene: CESP:Y A,Map position A;Introns: 43/	Query Match Best Local S Matches 18	3

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Prothetical protein alr0717 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: ACL896
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Cersion: ACL896
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <KUR>A;Residues: 1-225 <KUR>A;Residues: UNFROT:Q8YXX5; GB:BA000019; PIDN:BAB72674.1; PID:g17130062; GSPDB:GR

A; Gene: alr0717

Query Match

DB 2; 34.1%; Score 60;

Length 225;

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R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for odd
A;Reference number: A23701; MUID:91191556; PMID:1840504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for odd
A;Reference number: A23701, MUID:91191556; PMID:1840504
A;Accession: B37286
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer, Nature 361, 353-356, 1993
Nature 361, 353-356, 1993
A.Fitle: Cloning and expression of odorant receptors.
A.Reference number: S29707; MUID:93149273; PMID:7678922
A.Accession: S29707
                                                                                                                                                                                     A, Modecule type: mRNA
A, Residues: 1-314 < BNC>
A, Residues: 1-314 < BNC>
A, Cross-references: UNIPROT: P23272; GB: M64388; NID: 9205837; PIDN: AAA41751.1; PID: 9205838
C, Superfamily: olfactory receptor OR14
C, Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:076054; GB:AL096881
C;Comment: This protein has the following properties: (i) alpha-tocopherol specific bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: JC7708

R;Yamauchi, J.; Iwamoto, T.; Kida, S.; Masushige, S.; Yamada, K.; Esashi, T.
Blochem: Biochem: Diophyer, Res. Commun. 285, 295-299, 2016.
A;Title: Tocopherol-associated protein is a ligand-dependent transcriptional activator.
A;Reference number: JC7708; MUD:21338208; PMID:11444841
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               olfactory receptor OR5 - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C.Accession: S29707; #37286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tocopherol associated protein - human
NiAlternate names: alpha-tocopherol associated protein
C.Species: Homo sapiens (man)
C.Species: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 193-236 <BUC>
A;Cross-references: GB:M64375; NID:G205811; PIDN:AAA41738.1; PID:G205812
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                              30.4%; Score 53.5; 'DB 2; Length 314; 40.7%; Pred. No. 11; tive 5; Mismatches 4; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
30.4%; Score 53.5; DB 2; Length 314;
Best Local Similarity 40.7%; Pred. No. 11;
Matches 11; Conservative 5; Mismatches 4; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PRILIQNOQOHLPALP----IWFLL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PRILQNQQQHLPALP----IWFLL 24
                                                                                                                                    A, Accession: H23701
A, Status: nucleic acid sequence not shown
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A,Residues: 1-314 <RAM>
A,Cross-references: UNIPROT:Q04059
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 40.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-403 < YAM>
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: T00333
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. DNA Res. 5, 31.39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A;Reference number: Z14086; MUID:98290545; PMID:9628581
                                                                                                                                                                                                                                                                                                                                                                                                                                             RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature, 470-487, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                              hypothetical protein VCA0173 [imported] - Vibrio cholerae (strain N16961 serogroup O1) CiSpecies: Vibrio cholerae (state: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C.Accession: F82493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1421 <NAG>
A;Cross-references: UNIPROT:060306; EMBL:AB011132; NID:d1185402; PIDN:BAA25486.1
A;Experimental source: brain; clone HH1648
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C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: H23701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Species: Homo sapiens (man)
C,Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
                                              Gaps
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Pred. No. 31;
7; Mismatches 9; Indels
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                                              Indels
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RGLOSNSQHLPVVPTAKALPLWL----LRLHSI 116
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A;Molecule type: mRNA
                                                                                                      6 RLLQNQQQHLP-----ALPIWFLLQWLRLHPL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB;
Pred. No. 3.5;
0; Mismatches
             45.5%; Pred. No. 1.1; tive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein KIAA0560 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.2%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.2%;
Best Local Similarity 42.9%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 HLPALPIWFLLQW 26
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.2
Best Local Similarity 69.2
Matches 9; Conservative
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         Best Local Similarity
Matches 15; Conserv
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A; Gene: VCA0173 Genetics

à g A; Note: KIAA0560

RESULT 5

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CjAccession: 199558
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; MotCession: 199558
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Mucleic Acida Rea. 29, 2144-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90558
A;Accessions: 1-292 ACMR>
A;Accessions: I.292 ACMR>
A;Coss-references: UNIPROT:098021; GB:AL445566; PID:g14089784; PIDN:CAC13543.1; GSPDB:GRAExperimental source: strain UAB CTIP
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R;Purnalle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

B;Rurnalle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

A;Reference number: Z21823

A;Reference number: Z21823

A;Status: T38996

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: 1-862 - FURS

A;Cose-references: UNIPROT:O94441; EMBL:AL034583; PIDN:CAA22583.1; GSPDB:GN00066; SPDB:£

A;Experimental source: strain 972h-; cosmid c637
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A;Molecule type: DNA
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40988
R;Lyne, M; Rajandram, MA; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SPAC637.04 - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
        Species: Mycoplasma pulmonis
Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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Pred. No. 16;
1; Mismatches
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Pred. No. 47;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 LLKNSYEHPPSYPIKFLLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LLQNQQQHLPALPIWFLLQ 25
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ilarity 52.6%;
Conservative
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52.9%;
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Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity
Matches 10; Conserv
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A; Introns: 3/3; 41/1
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A;Genetic code: SGC3
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C;Date: Nostoc sp. FCZ 7120 is a synonym of Anabaena sp. strain FCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AB2475

B;Kanneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; Alitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: AB2475

A;Accession: AB2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q8YLE4; GB:BA000019; PIDN:BAB77053.1; PID:g17134493; GSPDB:GA;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: hglD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
13134
hglD protein - Anabaena sp. (fragment)
C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31334
R;Bauer, C.C.; Scappino, L.; Haselkorn, R.
Submitted to the EMBL Data Library, August 1994
A;Description: Heterocyst differentiation involves a new variant of polyketide or fatty
A;Reference number: Z21001
A;Accession: T31334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q44221; EMBL:U13677; NID:9538374; PID:9538375; PIDN:AAA93154
C;Genetics:
A;Gene: hglD
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B90558
hypothetical protein MYPU_3700 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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criptional activation involved in gene regulation in vivo in mammalian cells. C;Genetics:
A;Gene: tap
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                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 448;
                                                                                                                                                                       Length 403
                                                                                                                                                                                                                                                 Indels
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29.8%; Score 52.5; DB 2;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 12; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                        8 LSPROKEALAKFRENVODVLPALPNPDDHFLLRWLR 43
                                                                                                                                                                                                                                                                                                                           3 LOPR-----LLONQOHLPALP---IWFLLOWLR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-448 <BAU>
                                                                                                                                                               Score 53; DB 2;
Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTIEPAVAELLONODFHLAALP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTIEPAVAELLONODFHLAALP 157
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                                                                                                                                                                   Query Match 30.1%;
Best Local Similarity 44.4%;
Matches 16; Conservative
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Best Local Similarity 54.5'
Matches 12, Conservative
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A;Molecule type: DNA
A;Residues: 1-453 <KUR>
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C;Date: 22-Jan.1993 #sequence_revision 22-Jan.1993 #text_change 09-Jul-2004
C;Date: 22-Jan.1993 #sequence_revision 22-Jan.1993 #text_change 09-Jul-2004
C;Date: 22-Jan.1993 #sequence_revision 22-Jan.1993 #text_change 09-Jul-2004
R;Buck, L., Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od A;Reference number: A23701; MUID:91191556; PMID:1840504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-314 <BUC>
A;Cross-references: UNIPROT:P23274; GB:M64392; NID:g205845; PIDN:AAA41755.1; PID:g205846
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: E75219
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcous abyssi genome sequence: insights into archaeal chromosome stru A;Beference number: A75001
A;Accession: E75219
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A;Experimental source: strain Orsay
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    olfactory receptor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S20571
R;Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;
Nature 355, 453-455, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA
                                                          'n
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                          Gaps
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     DB 2; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lypothetical protein PAB2167 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 219,
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29.0%; Score 51; DB 2;
Best Local Similarity 31.8%; Pred. No. 16;
Matches 7; Conservative 9; Mismatches 6
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Pred. No. 20;
7; Mismatches
29.3%; Score 51.5; D
ilarity 48.1%; Pred. No. 15;
Conservative 3; Mismatches
                                                                                                                                           50 RTLIPAMLINMQ---PSLAIW--LHWI 71
                                                                                                         1 RILOPRILONGOOHLPALPIWFLLOWL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LLQNQQQHLPALPIWFLLQWLR 28
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Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PRILIQNOQOHLPALP
  Query Match
Best Local Similarity
Matches 13; Conserv
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A;Molecule type: DNA
A;Residues: 1-219 <KAW>
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A,Title: Expression of members of the putative olfactory receptor gene family in mammalia A,Reference number: $20571; MUID:92131132; PMID:1370859 A,Accession: $20571
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A;Accession: \$20571
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-313 <PAR>
A;Rossidues: 1-313 <PAR>
C;Superfamily: 01factory receptor OR14
C;Superfamily: 01factory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Gaps . 0 Length 313; Indels Score 51; DB Pred. No. 23; 4; Mismatches 29.0%; Query Match Best Local Similarity 53.34 Matches 8; Conservative

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5 PRILONOCOHLPALP 19 Search completed: November 10, 2004, 13:40:45
Job time : 8:12953 secs

norv norv norv

rattus 1 rattus 1

Q9gwwe rattus norv P2377 rattus norv Q8vgil mus musculu Q8egil mus musculu Q8egi6 shewanella Q8ej54 pseudomonas P88913 human herpe P97871 mus musculu Q15835 homo sapien Q9apxi pseudomonas Aat00534 homo sapien

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

38.1%; Score 67; DB 2; Length 1360;
Best Local Similarity 47.4%; Pred. No. 4.2;
Matches 18; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-Bristol N2;
Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125461; AAK18995.1; -..
FMR; T39322; T33922.
FMS; P07996, 11651.
WormPep; YBA9A.2; CE21336.
FMICEPPO; PRO00894; TSP1.
FMEM; PF00090; TSP 1; FS-1.
FMEM; PRO0090; TSP 1; 5...
FMINTS; PRO105; TSP1; 5...
SMART; SM00209; TSP1; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 1360 AA; 144313 MW; 312B206B6D087C3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Bristol N.A.
COurtney (FIB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LOPRILONQOQHLPALPIWFL-----LOWLRLHPL 32
                                                                                                                                                                                                                                                                                                              PRT; 1360 AA.
                                                                                                                                                                                                                                        ALIGNMENTS
              Q9QWW8
OLF9_RAT
P70526
Q8VG11
Q8E906
Q8HG48
Q88J54
P88913
                                                                                                                                P97871
RK_HUMAN
                                                                                                                                                                          AAT00534
Q7N2F5
                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, L
01-07-2003 (TrEMBLrel. 25, L
Hypothetical protein Y8A9A.2.
ORFNames=Y8A9A.2;
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.;
Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Bristol N2;
4444411111111111111
                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
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Q9TYK4
                                                                                                                                                                                                                                                                                    RESULT 1
 Q9TYK4
                                                                                                                                                                                                                                                                                                                                 SOW SERVICE STREET STRE
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Q7mxz photochabdu
Q3408 coccysus er
008742 mus musculu
Q895E83 bradyrhizob
Q9bd61 homo sapien
Q9wm3 drosophila
Q9wm3 drosophila
Q9wm3 drosophila
Q86xx2 drosophila
Q7654 homo sapien
Cag30457 homo sapien
Q9213 rattus norv
Q913 arttus norv
Q615b2 homo sapien
Q615b2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caf65898 neurospor
Q7qv42 giardia lam
Q9%mz3 vibrio chol
Q8ef6 shewanella
060306 homo sapien
Q9udx3 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aao52677 homo sapi
Aah69641 homo sapi
Q99ms0 rattus norv
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09qzu3 mus musculu
07s5b3 neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9tyk4 caenorhabdi
Q7r1b4 giardia lam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  giardia lam
                                                                                                     November 10, 2004, 12:27:34 ; Search time 39.0743 Seconds (without alignments) 471.205 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                    1825181
                 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                  176
1 RTLQPRLLQNQQQHLPALPIWFLLQWLRLHPL 32
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        1825181 segs, 575374646 residues
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09MD83
09MD83
086NX2
086NX2
086NX2
08142 HUMAN
142 BOVIN
143 HUMAN
143 HUMAN
061SB2
06XCI7
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S144_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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Q7R1B4
Q8YXS
Q7MZX2
Q7MZX2
Q9W MOUSE
Q89FS3
Q89FS3
                                                                             OM protein - protein search, using sw model
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AAH69641
S142 RAT
Q867A0
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CAF05898
Q7QV42
Q9KMZ3
Q8EF60
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext
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seg length: 200000000
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544
1556
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                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                          Run on:
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Gaps

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q34086
Q34086;
                                                                        Q7MZX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                             RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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                                                                          DDACOOCCOOR DDATE TO THE SECOND OF THE SECON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L., "Draft sequence of the Giardia lamblia genome.", sequence of the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21595285; PubMed=11759840; MEDLINE=21595285; PubMed=11759840; MEDLINE=21595285; PubMed=11759840; Muritz T., Sasamoto S., Watanabe A., Irigunim M., Molk C.P., Kuritz T., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Makazaki M., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120."; EMBL, AP003583; BAB72674.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                    GLP 306 58193 60304.
Giardia lamblia ATCC 50803.
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
35.2%; Score 62, DB 2; Length 703;
Best Local Similarity 56.0%; Pred. No. 9.9;
Matches 14; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.1%; Score 60; DB 2; Length 225; 45.5%; Pred. No. 5.4; ative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7/20).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae, Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
,; AACB01000028; EAA41130.1; -.
IENCE 703 AA; 78310 MM; B7FF2CCE01F1810B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 AA; 24777 MW; 96E6DFE80F9EB66A CRC64;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                  703 AA
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                                                                                                                                  PRT;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=alr0717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.5'
Matches 15; Conservative
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=184922;
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SEQUENCE 225 AA;
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SEQUENCE FROM N.A.
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                                                                                                                              Q7R1B4
Q7R1B4;
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                                                                                        RESULT 2
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                 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Thiol:disulfide interchange protein dsbD (C-type cytochrome biogenesis protein cyc2) (Inner membrane copper tolerance protein).
Name-dsbD; OrderedLocueNames=plu4139, Photorhabdus luminescens (subsp. laumondii).
BRoteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
NCBL_TAXID=141679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A., Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F., Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S., Redigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V., Zouine M., Glaser P., Bomare N., Danchin A., Kunst F.; The genome sequence of the entomopathogenic bacterium Photorhabdus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDITHE=9455264; bubMed=8075835;
Avise J.C., Nelson W.S., Sibley C.G.;
"Why one-kilobase sequences from mitochondrial DNA fail to solve the Hoatzni phylogenetic enigma.";
Mol. Phylogenet. Evol. 3:175-184 (1994).
-I- FUNCTION: Component of the ubiquinol-cytochrome c reductase
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Archosauria, Aves, Neognathae, Cuculiformes, Coccyzidae, Coccyzus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interproj. | Inter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
Cytochrome b (Fragment).
Coccyzus erythropthalmus (Black-billed cuckoo).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
575 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome, Redox-active center.
SEQUENCE 575 AA, 64072 MW, CBEC7F61
PRT;
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MEDLINE=22957627; PubMed=14528314;
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PROSITE; PS00194; THIOREDOXIN; 1.
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Pfam; PF00085; Thioredoxin; 2.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 50.0
les 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINE-STBLIAGE.
STRAINE-STSTS16; PubMed=1129030;
MEDLINE-STSTS16; PubMed=129030;
Ravanat C., Morales M., Azorsa D.O., Moog S., Schuhler S., Grunert P.,
Loew D., Van Dorsselaer A., Cazenave J.P., Lanza F.,
"Gene clouing of rat and mouse platelet glycoprotein V: identification of megakaryocyte-specific promoters and demonstration of functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lincombin cleavage.";
Blood 89:3223-3262(1997).
-- FUNCTION: The GPIb-V-IX complex functions as the von Willebrand factor receptor and mediates von Willebrand factor-dependent platelet adhesion to blood vessels. The adhesion of platelets to injured vascular surfaces in the arterial direculation is a critical intitating event in hemostasis (By similarity).
-- SUBCELLULAR LOCATION: Type I membrane protein.
-- SIMILARITY: Contains 14 leucine-rich (ERR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                           cytochrome b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                            EMBL; U02266; AAAG5038.1; -... Grown of the control of the control
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                                                                                                                                                                              270 SLAPLIKNSKRAMPSRPLSQTLFWFLVENLFILKWLGSHPV 311
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320 AA; 35716 MW; B277E235154D235A CRC64;
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05-JUL-2004 (Rel. 44, Last annotation update)
Platelet glycoprotein V precursor (GPV) (CD42D)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57.5; 1
Pred. No. 17;
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15-JUL-1998 (Rel. 36, Last seq
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.7%;
31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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O08742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
NON TER
SEQUENCE
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GPV MOUSE

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OO Namma
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EMBL; Z65955; CAA93441.1; -.

R HSSP, Q9EZR6; 10ZN.

R HSSP, Q9EZR6; 10ZN.

R INCEPPO: IPRO01611; LRR_Cterm.

R INCEPPO: IPRO01631; LRR_Cterm.

R INCEPPO: IPRO053591; LRR_CYP.

R Ffam; PF00463; LRR_T; 13.

R Ffam; PF00463; LRR_T; 13.

R PFAM; SM00082; LRR_TYP.

R SWART; SM00369; LRR_TYP; 10.

R SWART; SM00369; LRR_TYP; 10.

R Hood coagulation, Cell adhesion, Glycoprotein; Leucine-rich repeat;

R SIGNAL

T GIGNAL

T DOMAIN

T S67

Platelet glycoprotein V.

T TRANSMEM 523

FOLEENIAL.

T DOMAIN

T TRANSMEM 523

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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C48643AA73967A7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PRILIQUOQUILPAL --- PIWFLLQWIRLHP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 57.5; 46.7%; Pred. No. 32
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N-linked
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385
567 AA;
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B116626 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=375;
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CARBOHYD
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REPEAT
REPEAT
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Q89FS3
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RESULT 8

Q9B214

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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jozenah H., Moore T., Max S.I., Wang J., Hashe F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Bronstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Willalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Rhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rheeley R.W. Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rraywinski M.I., Sakaska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
                   Eukaryoča; Metazoa; Chordata; Craniata; Vartebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Straubberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BCOS9915, AAHS8915.1,
R InterPro; IPR001251; CRAL_TRIO_N.
R InterPro; IPR001251; CRAL_TRIO_N.
R InterPro; IPR001071; RetBind/tocTrans.
R InterPro; IPR001074; Sc14p like_N.
R InterPro; IPR008983; TNF like_N.
R Pfan; PF003650; CRAL_TRIO_N.
R Pfan; PF003650; CRAL_TRIO_N.
R Pfan; PF00365; CRAL_TRIO_N.
R PRINTS; PR00180; CRETINALDHBP.
R PRINTS; PR00180; CRETINALDHBP.
R PROSTIE; PS50191; CRAL_TRIO; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
      sapiens (Human)
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                                                                                                        SEQUENCE FROM N.A.
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TD AAH58915
AC AAH58915
DT 02-MAR-200
DT 02-MAR-200
DT 02-MAR-200
DE Hypothetic
OS Hypothetic
OS Bukaryota,
OC Mammalia,
OX NOBITAXII
RN | 1]
RP SEQUENCE F
RC TISSUE=Bre
RX MEDLINE=Z
RA Strausberg
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                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Archosauria; Crocodylidae; Alligatorinae; Caiman.
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                                                                                                                     Ouery Match
32.4%; Score 57; DB 2; Length 111;
Best Local Similarity 39.3%; Pred. No. 6.5;
Matches 11; Conservative 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 32.4%; Score 57; DB 2; Length 352; Local Similarity 46.4%; Pred. No. 22; length 352; les 13; Conservative 3; Mismatches 8. Thank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
                                                                                 111 AA; 12601 MW; E2F95EF338B8BAB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion, NAD, Oxidoreductase, Ubiquinone.
SEQUENCE 352 AA, 38810 MW, 68197AA6DD36D8A3 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                 01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   352 AA.
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                                                                                                                                                                                                                                5 PRLLQNQQQHLPALPIWFLLQWLRLHPL 32
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InterPro; IPR010933; NaDH dehy_S2_C.
InterPro; IPR011093; NaDH dehy_S2_C.
Pfam; PF06444; NaDH dehy_S2_C; 1.
Pfam; PF00361; Oxidored_q1:1.
Bradyzhizobium japonicum USDAll0.";
DNA Res. 9:189-197(2002).
EMBL, APOGS59; BAC51891.1; -.
CCMplete proteome.
SEQUENCE 111 AA; 12601 MW; E2F95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21190842; PubMed=11297180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADH dehydrogenase subunit 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01436; NADHDHGNASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissue=Liver;
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Q6PD61;
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Matches
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7
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Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
                                                                                                                         10;
                                                                    32.4%; Score 57; DB 2; Length 392; 44.4%; Pred. No. 25;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB=Brain;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Hypothetical protein. --
SEQUENCE 392 AA, 44747 MW, 11A833345968FE5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                  392 AA.
                                                                                                                    3; Mismatches
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RESULT 9

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Q6PD61

Ketchum K.A.,

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Jalali
Kimmel
            A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hookins K.F., Jordan H., Moore T., Max S.I., Wang J., Habte F., Ab Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bronstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Frange C., And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunararne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Ay Villalon D.K., Muzuy D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Rodriguez A.C., Grimwood J., Schmutz J., McKernan J.W., Green E.D., Dickson M.C., Antara M.A., Young A.C., Shevchenko Y., Boutfard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Toung A.C., Smailus D.E., Schnerch A., Schein J.E., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Grimeration and initial analysis of more than 15,000 full-length human and mouse contact sequences.
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REDLINE=20196006; PubMed=10731132;

Madams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAdams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Gocaye R.A., Lewis S.E., Richards S.A., Abnurner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Randon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA MAR K.H., Doyle C., Baxerer E.G., Helt G., Melson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,

Rallew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

Rallew R.M., Buctchan M.R., Bouck J., Bockstein P., Botcher A., Chanta I.,

Rockova D., Botchan M.R., Bouck J., Botcher R., Center A., Chanta I.,

Rappenson K., Downey S., Dahlke C., Davenport L.B., Davies P.,

Rockov R., Downes M., Dugan-Rocha S., Pleischmann W.,

Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Rockow K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Rottin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroida; Drosophila, NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 32.4%; Score 57; DB 2; Length 392; Local Similarity 44.4%; Pred. No. 25; 7; Indels nes 16; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Brain;
Strausberg R.;
Submitted.(OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058915; AAH58915.1; -.
Hypothetical protein.
SEQUENCE 392 AA; 44747 WW; 11A833345968FE5A CRC64;
                                                                                                                                                                                                                                                                                                Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=CG13902;
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Kimmel B.E., Kodira C.D., Kraftz C., Neuritz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J. Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J. Li Z., Liang Y., Lin X.,
Liu X., Mattel B.E., McIntosh T.C., McLeod M.P., Morberson D.,
Merkulov G., Milshina N.V., Mobary C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ralson D.R., Nabson K.A., Nixon K., Nusskern D.M., Perloy D. Reinert K., Semington K., Saunders R.D., Scheeler F., Shen H.,
Reinert K., Femington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
Milliams S.M., Woodage T., Woiley K.C., Mu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
I'the genome sequence of Drosophila melanogaster.";
I'the genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Prise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.; Lewis S.E., Rubin G.M.,
"The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patels D.J.M., Pfeiffer B.D., Richards S., Sodergren E.J., Wichards S., Sodergren E.J., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESBARCH0079-RESBARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis S.E., "Annotation of the Drosophila melanogaster euchromatic genome: systematic review."; Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
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Pred. No. 25;
1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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FlyBaase; FBGM003166; CG13902.
InterPro; IPR007113; Cupin region.
InterPro; IPR003347; TF JMJC.
Pfam; PR02373; JMJC; 1.
SEQUENCE 394 AA; 44323 MW; 03E15F55F25EF503 CRC64;
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ilarity 54.2%;
Conservative
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Best Local Similarity
Matches 13; Conserv
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Q86NX2 Q86NX2;

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RESULT 12
086NXZ
AC 086NXZ
AC 086NXZ
AC 086NX
DT 01-JT
DT

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from size-fractionated cDNA libraries from human brain.";
DNA Res. 6:329-336(1999).
-!- FUNCTION: Carrier protein. Binds to some hydrophobic molecules and
                                                                                           pubmed=11226224; DOI=10.1073/pnas.041620398;
Shibbata N, Artita M., Misaki Y., Dohmae N., Takio K., Ono T.,
Inoue K., Arai H.,
"Supernatant protein factor, which stimulates the conversion of
squalene to lanosterol, is a cytosolic squalene transfer protein and
enhances cholesterol biosynthesis.";
Proc. Natl. Acad. Sci. U.S.A. 98:2244-2249(2001).
Tocopherol-associated protein is a ligand-dependent transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20039618; PubMed-10574461;
Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
Collins J.E., Huckle E.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION
                   ctivator.";
iochem. Biophys. Res. Commun. 285:295-299(2001).
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                     activator
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076054; OPULN4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
SEC14-like protein 2 (Alpha-tocopharol associated protein) (TAP)
(HTAP) (Supernatant protein factor) (SPF) (Squalene transfer protein)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLINE=21338208; PubMed=11444841; DOI=10.1006/bbrc.2001.5162;
Mamauchi J., Iwamoto T., Kida S., Masushige S., Yamada K., Esashi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawpe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20400504; PubMed=10829015; DOI=10.1074/jbc.M000851200;
Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Sassoon J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A novel human tocopherol-associated protein: cloning, in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Endopteraygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.4%; Score 57; DB 2; Length 401; 54.2%; Pred. No. 26; cive 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), ALTERNATIVE SPLICING, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AA; 45199 MW; 8380B46D7BF05032 CRC64;
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                                                                                                                                                              Last sequence update)
                                                                                                                 401 AA
                             176 QPTLLLNTIQHWPALHKWLDLNYL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 QPTLLLNTIQHWPALHKWLDLNYL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression, and characterization."; J. Biol. Chem. 275:25672-25680(2000).
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      27
                                                                                                                                                Created)
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FlyBase; FBgn0035166, CG13902.
InterPro; IPR007113; Cupin region.
InterPro; IPR003347, TF_JmJC.
Pfan; PF02273; JmjC, 1.
SWART; SM00558; JmjC, 1.
      OPRLIQUOQOHLPALPIWFLLOWL
                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                            ORFNames=CG13902;
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                                                                                                                                                                                               GM21055p.
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SEQUENCE Query Match

Matches

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MIM; 607558; -.

DR GO; GO:0005737; C:Cytoplasm; NAS.

DR GO; GO:0005737; C:Cytoplasm; NAS.

DR GO; GO:0005543; F:phospholipid binding; NAS.

DR GO; GO:0005543; F:phospholipid binding; NAS.

DR GO; GO:0005543; F:phospholipid binding; NAS.

DR GO; GO:000563; F:ranascriptional activator activity; NAS.

DR GO; GO:0045893; P:positive regulation of transcription, DNA-d.

DR HIGEPTO; IPRO01251; CRAL_TRIO_O.

DR InterPro; IPRO01071; RetBind/tocTrans.

DR InterPro; IPRO01071; RetBind/tocTrans.

DR InterPro; IPRO01803; TNF 1ke.

DR Pfam; PFO0550; CRAL_TRIO_f.

DR PRINTS; PRO0180; CRETINALDHBP.

DR PROSITE; PSSO191; CRAL_TRIO; 1.

DR PROSITE; PSSO191; CRAL_TRIO; 1.

DR PROSITE; PSSO191; CRAL_TRIO; 1.

DR PROSITE; PSSO191; Transcription regulation; Transport.

FUNDAIN

FUNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.cib.ch)
promotes their transfer between the different cellular sites. Binds with high affinity to alpha-tocopherol. Also binds with a weaker affinity to other tocopherols and to tocotrienols. May have a transcriptional activatory corpierols and to tocotrienols. May have a transcriptional activatory corporates and binds some squalene structure, suggesting that it may regulate cholesterol biosynthesis by increasing the transfer of squalene to a metabolic subsunt: Monomer (By similarity).

SUBCELULAR LOCATION: Cytoplasmic in absence of alpha-tocopherol, and nuclear in presence of alpha-tocopherol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=3;
IsoId=076054-3; Sequence=Not described;
TISSUE SPECIFICITY: Widely expressed. Strong expression in liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain and prostate.
-!-DEVELOPMENTAL STAGE: Low expression in fetal tissues.
-!-SIMILARITY: Contains 1 CRAL-TRIO domain.
-!-SIMILARITY: Contains 1 GOLD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (in isoform 2).
/FTId=VSP 006031.
Y -> H (in Ref. 2).
D846747EC8D1513E CRC64;
                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                   Name=2;
IsoId=076054-2; Sequence=VSP_006031;
                                                                                                                                                                                                                                                                                                                                                                          IsoId=076054-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL096881; CAB51405.1; -. EMBL; AC04832; AAF19256.1; -. EEMBL; AB033012; BAA86500.1; -. PIR; JC7708; JC7708. PDB; 106U; X-ray; A/C/E=1-403.
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403 AA; 46145 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383
403
                                                                                                                                                                                                                                                                                                                                                    Name=1;
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Meadus J., MacInnis R., Dubeski P., Hidiroglou N., Madere R.;
"Induction of hepatic tocopherol associated protein (TAP) mRNA but no:
alpha-tocopherol transfer protein (TTP) mRNA in cattle fed increasing
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEGUENCE OF 178-195 AND 335-353.
MEDLINE-20400504; PubMed=10829015; DOI=10.1074/jbc.M000851200;
Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Sassoon J.,
                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A,
Coll C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y., Huckle E
Bear D.M., Dunham I.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR456571; CAG30457.1;
SEQUENCE 403 AA; 46145 MW; D846747EC8D1513E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP)
(bTAP) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                            Query Match 32.4%; Score 57; DB 2; Length 403; Best Local Similarity 44.4%; Pred. No. 26; Matches 16; Conservative 3; Mismatches 7; Indels
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                                                                                                                                Last sequence update)
Last annotation update)
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               3 LOPR----LLQNQQQHLPALP---IWFLLQWLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                 403 AA.
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                                                                                                                    Created)
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                                                                                                                  01-JUN 2004 (TrEMBLrel. 27, 01-JUN-2004 (TrEMBLrel. 27, 01-JUN-2004 (TrEMBLrel. 27, SEC14L2 protein.
                                                                                         PRELIMINARY;
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NCBI_TaxID=9913;
                                                                                                                                                                                                                           NCBI_TaxID=9606;
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P58875;
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                                                                                            CAG30457
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S142 BOVIN
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32.4%; Score 57; DB 1; Length 403; 44.4%; Pred. No. 26; ive 3; Mismatches 7; Indels

Conservative

Best_Local Similarity Matches 16; Conserv

Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                           structure, suggesting that it may regulate cholesterol
blosynthesis by increasing the transfer of squalene to a metabolic
active pool in the cell (By similarity).
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Cytoplasmic in absence of alpha-tocopherol, and nuclear in presence of alpha-tocopherol (By similarity).
-!- SIMILARITY: Contains 1 GOLD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                       44406 MW; FAE72E8A83CB9E9C CRC64;
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SEQUENCE
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Search completed: November 10, 2004, 13:38:39 Job time : 41.0743 secs

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Gaps

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DB 1; Length 387; 4; Indels

Query Match
32.1%; Score 56.5; D:
Best Local Similarity 56.5%; Pred. No. 29;
Matches 13; Conservative 3; Mismatches

9 QNQQQHLPALP --- IWFLLQWLR 28

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12, Appl
14886, B
2, Appli
2, Appli
2, Appli
38576, B
14171, B
18690, B
483178, B
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19500, A
61329, A
9, Appli
45804, A
18106, A
13147, A
2, Appli
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Sequence 15547, A
Sequence 27928, A
                                                                        November 10, 2004, 12:32:37; Search time 12.7807 Seconds (without alignments)
191.991 Million cell updates/sec
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1. /cgn2 6/ptodatea/1/iaa/5A_COMB.pep:*

2. /cgn2 6/ptodatea/1/iaa/5B_COMB.pep:*

3. /cgn2 6/ptodatea/1/iaa/6A_COMB.pep:*

4. /cgn2 6/ptodatea/1/iaa/6B_COMB.pep:*

5. /cgn2 6/ptodatea/1/iaa/PCTUS COMB.pep:*

5. /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*

5. /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
                                                                                                                                                      1 MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSFTP 37
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-248-796A-15547

US-09-248-796A-2928

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US-09-848-796A-14886

US-08-212-188-2

US-08-970-722-2

PCT-US95-02708-2

US-09-270-767-38576

US-09-270-767-38793

US-09-228-796A-1471

US-09-228-796A-1471

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US-08-455-543A-55
US-08-223-305C-55
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                                                                                                                                                                                                                       478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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187
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Sequence 15547, Application US/09248796A

Sequence 15547, Application US/09248796A

Sequence 15547, Application US/09248796A

Batterl No. 6747133.

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.13

CURRENT APPLICATION NUMBER: US 60/094,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15547

IINELSQRDSCGPLKISLNNKILVYGNLF 32 :|| | : :||:|||| : VINHLDSPGLAGMICRRINNRILLVYGGSY 33

US-09-248-796A-15547

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Sequence 56, Appl Sequence 54, Appl Sequence 54, Appl Sequence 25, Appl Sequence 22, Appl Sequence 52, Appl Sequence 52, Appl Sequence 4, Appl Sequence 4, Appl Sequence 17, Appl Sequence 53, Appl Sequence 2963, Appl Sequence 19923, Appl Sequence 19923, Appl Sequence 19923, Appl Sequence 2663, Appl	1 Sequences Relating to Streptococcus	Length 307;
US-08-455-543A-56 US-08-223-305C-56 US-08-455-543A-54 US-08-223-305C-54 US-08-223-305C-54 US-08-233-305C-52 US-08-233-305C-52 US-08-233-305C-52 US-08-713-118-4 US-09-452-007-4 US-09-452-007-4 US-09-455-43A-53 US-09-55C-818-60 US-09-55C-818-60 US-09-55C-818-60 US-09-55C-818-60 US-09-55C-818-60 US-09-58-796A-19923 US-09-438-376-2	GNMENTS O d Amino Acic biagnostics 3,110 ,433 ,131	Score 53; DB 4; Pred. No. 3.8;
10084 100884 10086 10086 10091 11009 11009 11009 11009 11009 11009 11009 11009 11009 11009 11009 11009 11009 11009 11009 11009	4473 73, Application US/095831. 78, Application US/095831. 26899703. Lynn Doucette-Stamm et . Lynn Doucette-Stamm et . Lynn Doucette-Stamm et . VNENTION: Nucleic Acid a. VNENTION: Nucleic Acid a. VNENTION: Doucette-Stamm et . NUCLEIC DOUCET . 2000-05-26 LING DATE: 2000-05-26 ICATION NUMBER: US 60/08 NG DATE: 1998-06-30 ICATION NUMBER: US 60/08 NG DATE: 1998-05-12	28.3%;
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ALIT 109-583-110-4473 Sequence 4473, Application US/0958311 PATENT NO. 6699703 APPLICANT: Lynn Doucette-Stamm et a TITLE OF INVENTION; Nucleic Acid an TITLE OF INVENTION; Nucleic Acid an TITLE OF INVENTION; Phemoniae for FILE REFERENCE: PATHO0-07A CURRENT APPLICATION NUMBER: US/09/58 CURRENT APPLICATION NUMBER: US 60/085 PRIOR APPLICATION NUMBER: US 60/085 PRIOR PLING DATE: 1998-06-30 PRIOR PLING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/085 PRIOR APPLICATION NUMBER: US 60/081 PRIOR PLING DATE: 1998-06-10 PRIOR FILING DATE: 1998-06-17 PRIOR PLING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: US 60/081 PRIOR PLING DATE: 1998-06-17 PRIOR PLING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: US 60/081 PRIOR PLING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: US 60/081	/ Match Local Similarity
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	RESULT 1 US-09-53-110-4473 Sequence 4473, App Patent No. 6699703 GENERAL INFORMATION TITLE OF INVENTION FILE REFERENCE: CURRENT APPLICATION FRIOR PILING DATE PRIOR APPLICATION PRIOR PILING DATE PRIOR FILING DATE PRIOR PILING DATE TYPE: PRT CREANISM: SIEEPT CREANISM: SIEETT CREANISM: S	Query Match

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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANTION: UCULBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
SEQ ID NOS: 28208
SEQ ID NO 14886
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Pred. No. 38;
3; Mismatches 18; Indels
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Sequence 2, Application US/08212188

Patent. No. 5689019

GENERAL INFORMATION:
APPLICANT: BECKER, JEFFREY M.
APPLICANT: STACEY, GARY
TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: HOWERY & SIMON
STREET: 1299 PERNNSYLVANIA AVE., N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,188
FILING DATE:
FLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AUGRAACH, JEFFREY I
REGISTRATION NUMBER: 32,680
REFRENCE/POCKET NUMBER: 32,680
REFRENCE/POCKET NUMBER: 37,980
TELEBEHONE: (202) 383-7451
                                                       1 MAVIINELSQRDSCGPLKISLNNKIL 26
                                                                                                                                                                                                                                                             US-09-248-796A-14886
; Sequence 14886, Application US/09248796A
; Patent No. 6747137
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Best Local Similarity 39.0%;
Matches 16; Conservative 3
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TELEFAK: (202) 383-610
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 610 amino acids TYPE: amino acid TOPOLOGY: inhear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Candida albicans
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                    DB 4; Length 904;
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                                                                                                                                                                                                                    Query Match 28.3%; Score 53; DB Best Local Similarity 41.7%; Pred. No. 16; Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 DSCGPLKISLNNKILVYGNLFSSF 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Staphylococcus aureus US-09-830-217-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.4%;
Matches 12; Conservative 6
; LENGTH: 904
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Candida albicans
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Best Local Similarity
Matches 9; Conserv
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PLANT PEPTIDE TRANSPORT GENE
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ORGANISM: Arabidopsis thalliana
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, UBFREY I
REGISTRATION NUMBER: 32,680
REFRENCE/DOCKET NUMBER: 7493-
TELEPHONE: (202) 383-7451
TELEPHONE: (202) 383-610
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Drosophila melanogaster
US-09-270-767-38576
    JEFFREY M.
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Best Local Similarity 34.4%;
Matches 11; Conservative
    APPLICANT: BECKER, JEFFRE
APPLICANT: STACEY, GARY
TITLE OF INVENTION: PLANT
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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PCT-US95-02708-2
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                                                                                                                                                                             Score 49; DB 1; Length 610
Pred. No. 42;
9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08970725
; Sequence 2. Application US/08970725
; Patent No. 6080542
; GENERAL INFORMATION:
    APPLICANT: Stacey, Gary
    TILE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
    NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: WISER & ASSOCIATES
    STREET: 230 South Fifteenth Street, Suite 500
    STREET: Philadelphia
    STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,725
FILING DATE: 14-NOV-1997
CLASSIFICATION NUMBER: US 08/212,188
APPLICATION NUMBER: US 08/212,188
APPLICATION NUMBER: US 08/212,188
APPLICATION NUMBER: US 08/212,188
REGISTRACTION NUMBER: 19,763
                                                                                                                                                                                                                                                                                             5 INELSQRDSCGPLKISLNNKILVYGNLFSSFT 36
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thalliana
IMMEDIATE SOURCE:
CLONE: ATPTR2AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
PCT-US95-02708-2
PCT-Gequence 2, Application PC/TUS9502708
; SEGNERAL INPORMATION:
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TELEPHONE: 215-875-838
TELEPHONE: 215-875-8394
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             26.2%;
34.4%;
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                                                                                                                                                                        Query Match
Best Local Similarity 34.4°
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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Matches 11; Conserv
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US-08-212-188-2
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITIE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE OF INVENTION: Nucleic 326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
ERGTH: 160
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Pred. No. 42;
9; Mismatches 12; Indels
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                                                                                                                   CONFUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02708
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LSQRDSCGPLKISLN----NKIL----VYGNLFSSF 35 : | | | | | | | | | | | | | | |
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SSEE: HOWREY & SIMON
1: 1299 PENNSYLVANIA AVE., N.W.
WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-270-767-38576
; Sequence 38576 Application US/09270767
; Patent No. 6703491
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 48395

LENGTH: 151
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                                                                                                                                                                                                                                                                                  Query Match 25.7%; Score 48; DB 4; Length 414; Best Local Similarity 32.1%; Pred. No. 36; Astches 9; Conservative 7; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
25.4%; Score 47.5; D
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa means any amino acid
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145 LALVLEDLFPRDGLGPLHAELGRAMHVF 172
                                                                                                                                                                                                                                                                                                                                                                                                 1 MAVIINELSQRDSCGPLKISLNNKILVY 28
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US-09-270-767-48395
Sequence 48395, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 RDSC----GPLKISLNNKILVYG 29
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ORGANISM: Drosophila melanogaster
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                                                                                                                                                                       TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18690
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33178
LENGTH: 151
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US-09-270-767-33178
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US-09-248-796A-14171
US-09-248-796A-14171
Sequence 14171, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR PRIDGE APPLICATION NUMBER: US 60/074,725
FRIOR FILING DATE: 1998-02-13
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR SEQ ID NOS: 28208
SEQ ID NO 14771
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABEUGINOSA FOR DIAGNOSTICS AND THERRAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                                                                                                          APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: NUCLEIC 1226-034
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 53793
LENGTH: 160
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25.7%; Score 48; DB 4; Length 336;
Best Local Similarity 33.3%; Pred. No. 27;
Matches 11; Conservative 6; Mismatches 16; Indels
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        3 VSMADNCGNLRLSMNELSGNEYLPSANAYGMQYEDF 38
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                            Sequence 53793, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-18690
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                                                                                      RESULT 10
US-09-270-767-53793
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RESULT 15

US-09-248-796A-14928

US-09-248-796A-14928

Sequence 14928, Application US/09248796A

FAPELGART RELATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/0948, 796A
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR PILING DATE: 1998-08-13
FRIOR PILING DATE: 1998-08-13
FRIOR FILING DATE: 1998-08-13
FRIOR FILI
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25.4%; Score 47.5; DB 4; Length 308;
Best Local Similarity 44.4%; Pred. No. 29;
Matches 12; Conservative 4; Mismatches 4; Indels 7
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RESULT 1
US-10-092-750-38
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Sequence 5855, Ap
Sequence 10198, Ap
Sequence 4173, Ap
Sequence 311744,
Sequence 267293,
Sequence 36925, A
Sequence 311741,
Sequence 318064,
Sequence 280511,
Sequence 28051,
                                                                                                                    November 10, 2004, 16:36:12; Search time 39.7478 Seconds (without alignments) 328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

1. 'Cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2. 'Cgn2_6/ptodata/1/pubpaa/DTO7_NEW_PUB.pep:*
3. 'Cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4. 'Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5. 'Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
7. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19. 'Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19. 'Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
19. 'Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
19. 'Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
20. 'Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
                                                                                                                                                                                                                                              1 MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSFTP 37
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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15 US-10-282-122A-78432

14 US-10-369-493-5855

14 US-10-369-493-10198

19 US-09-738-626-473134

17 US-10-425-115-267293

17 US-10-425-115-65025

17 US-10-425-115-311741

15 US-10-425-115-311741

15 US-10-425-115-311741

17 US-10-425-115-311741

18 US-10-425-115-311741

19 US-10-425-115-18664

11 US-10-425-115-18664

12 US-10-425-115-18664
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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187
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Match Length DB
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Seguence 119330,	a	ednence		Seguence 12, Appl	Sequence 44313, A	ednence	Sequence 131078,	ednence	equence	Sequence 173672,	ednence	Sequence 161016,	ednence	Sequence 195520,	Seguence 78, Appl	Seguence 79, Appl	Sequence 227072,	Sequence 192381,	(I)	Sequence 133, App	(I)	Sequence 35254, A	Sequence 3649, Ap	ednence	Sequence 305381,	ednence	Sequence 38, Appl	a)	e 14	e 14	Sequence 170853,
-437-963-11933	US-10-282-122A-53155	US-09-815-242-12577	US-09-815-242-5223	US-10-278-946-12	US-10-282-122A-44313	US-10-424-599-221825	US-10-437-963-131078	US-10-437-963-179710	5 US-10-437-963-156545	US-10-424-599-173672	US-10-437-963-158688	US-10-437-963-161016	US-10-292-798-1024	US-10-437-963-195520	US-10-252-734-78	US-10-252-734-79	US-10-424-599-227072		US-10-424-599-183247	US-09-860-670-133	US-10-227-646-133	US-10-767-701-35254	US-10-108-260A-3649	US-10-786-720-56	US-10-425-115-305381	US-10-425-114-53217	US-10-166-087-38	US-10-425-115-288866	US-10-437-963-143504	US-10-437-963-143585	US-10-424-599-170853
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523	662	664	691	691	691	114	807	991	1051	168	578	115	264	483	33	33	41	83	105	203	203	226	333	333	340	345	347	733	926	1283	152
26.7	26.7	26.7	26.7	26.7	26.7	26.5	26.5	26.5	26.5	26.2	26.2	25.9	25.9	25.9	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.4
20	20	20	20	20	20	49.5	49.5	49.5	49.5	4	4,00	48.5	48.5	48.5	48	48	48	48	48	48	48							48			47.5
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	. 45

ALIGNMENTS

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100.0%; Score 187; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 37; Conservative 0; Mismatches 0; Indels
Sequence 38, Application US/10092750
; Sequence 38, Application US/20092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
    APPLICANT: Hammond, Philip W.
    APPLICANT: Alpin, Julia
    APPLICANT: Mright, Martin C.
    ITILE OF INVENTION: Polypeptides Interactive with BCL-X1
    FILE REFERENCE: 50036/050002
; CURRENT FILING DATE: 2002-03-07
    PRIOR PAPLICATION NUMBER: US 60/274,526
; RIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-092-750-38
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Gaps

RESULT 2
US-10-289-122A-78432
Sequence 78432, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

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Gaps

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Sequence 10198, Application US/10369493
; Sequence 10198, Application US/10369493
; Publication No. US20030233675A1
GENERAL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
; APPLICANTION: EXPRESSION OF MICROBIAL PROPERTIES
; FILE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; FILE OF INVENTION: BARRY BARRY S.
; CURRENT APPLICATION NUMBER: US 60/369, 493
; CURRENT PILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10198
                                                                                                                                                          Score 55; DB 14; Length 619;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.9%; Score 54; DB 14; Length 324; Best Local Similarity 41.2%; Pred. No. 15; Matches 14; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                               4; Mismatches
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GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: HAYBASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATELSHI, NAKOKO
APPLICANT: TENDA, MASATO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT FILING DATE: 200-12-18
CURRENT FILING DATE: 200-12-18
                                                                                                                                                                                                                                                                                                                                      238 GEYSVDGKSLYYGNMMSDVTP 260
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                         15 GPLKISLNNKILVYGNLFSSFTP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4773, Application US/09738626
Publication No. US20020197605A1
                                                             ) ORGANISM: Caenorhabditis elegans
US-10-369-493-5855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10198
                                                                                                                                                          Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-10-369-493-10198
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LENGTH: 619
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ORGANISM:
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Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: ABLER.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, USABESION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(5052)B I UNDER: US/0/369, 493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APLICATION NUMBER: 06/191,078

PRIOR APPLICATION NUMBER: 60/202,

PRIOR APPLICATION NUMBER: 60/203,21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/203,727

PRIOR APPLICATION NUMBER: 60/203,347

PRIOR APPLICATION NUMBER: 60/203,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-30

PRIOR FILING DATE: 2001-13-30

PRIOR FILING DATE: 2001-13-30
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                                                                                            Haselbeck, Robert
Ohlsen, Kari
                                                                                                                                                                                                                                                       Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.04
Matches 13; Conservative
                              Zamudio, Carlos
Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Yersinia pestis
US-10-282-122A-78432
                                                                                                                                                                                                                               Trawick, John
   Wang, Liangsu
                                                                                                                                                                                            Wall, Daniel
                                                                                                                                                                 Zyskind,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Gaps

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**Sequence 311741, Application US/10425115
**Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSa, Thomas J.
APPLICANT: Cabou, Yihua
A
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 39-21 (53313) B
CURRENT FILING DATE: 2003 04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 65225
LENGTH: 358
              Gaps
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       7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.5%; Score 51.5; DB 15; Length 358; Best Local Similarity 34.4%; Pred. No. 42; Aatches 11; Conservative 7; Mismatches 7; Indels 7.
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION; Clone ID: LIB3606-010-G12_FLI.pep
US-10-425-114-65925
           11;
                                                                                                                               28 LVVGTTSLAQSSSLGPLRISPWNK-----STSFTP 57
                                                                              1 MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSFTP 37
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US-10-425-115-311741
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                                                                                                                                                                                                                                                                                            US-10-425-114-65925
Sequence 65925, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
              4;
           15; Conservative
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ORGANISM: Zea mays
FEATURE:
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-10-425-115-311741
              Matches
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yondai
APPLICANT: Cao, Yondai
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 311744
LENGTH: 122
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FUBLICATION NO. US20040214272A1
FUBLICANT: LA ROBA. Thomas J.
APPLICANT: La Robalt, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE REFERENCE: 38-21(5322)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 267293
LENGTH: 158
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                                                                                                                                                                                                                                                  Query Match 27.8%; Score 52; DB 9; Length 755; Best Local Similarity 35.3%; Pred. No. 88; Matches 12; Conservative 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Clone ID: NRT4577_175373C.1.pep
US-10-425-115-267293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_47363C.1.pep
US-10-425-115-311744
                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VIINELSQRDSCGPLKISLNNKILVYGNLFSSFT 36
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                                                                       i LENGTH: 755
TYPE: PRT
; ORGAN:SM: Corynebacterium glutamicum
US-09-738-626-4773
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SOFTWARE: Patentin ver. 3.0
SEQ ID NO 4773
LENGTH: 755
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Best Local Similarity
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ORGANISM: Zea mays
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US-10-425-115-267293
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Zhou Yihua

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             Sequence 64080, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION;

APPLICANT: Litu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Avoil C. David K.

APPLICANT: Tabaska, Jack E

APPLICANT: ANOTHER SCREEN STORGER

APPLICANT: Tabaska, Jack E

APPLICANT: ANOTHER SCREEN STORGER

APPLICANT: ANOTHER SCREEN STORGER

COURENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 441
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Publication No. US20040214272A1
GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APP
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US-10-425-114-64080
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; OTHER INFORMATION: Clone ID: MRT4577_112213C.1.pep
WS-10-425-115-198064
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27.5%; Score 51.5; Di
Best Local Similarity 34.4%; Pred. No. 54;
Matches 11; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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Best Local Similarity
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ORGANISM: Zea mays
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US-10-425-115-198064
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US-10-425-114-64080
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APPLICANT: Li, Ping Tries Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 66
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US-10-424-599-280511
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US-10-437-963-126350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 LIHSPSITRSCKPFYIWPGTQILHYSNYFGFTSKFTP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
26.7%; Score 50; DB 16;
Best Local Similarity 30.8%; Pred. No. 31;
Matches 12; Conservative 8; Mismatches 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 126350, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Barbacut, Nei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbacut, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 119330, Application US/10437963
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Rovalic, David K.
; APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                 ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-10-437-963-119330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-10-437-963-126350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 126350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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APPLICANT: Li, 2199
TITLE OF INNENTION: Plates and Uses Teaced for Plant Improvement
TITLE OF INNENTION: Plates and Uses Teaced for Plant Improvement
TITLE OF INNENTION: Plates and Uses Teaced for Plant Improvement
CHESTER TRANSCHIPS 19.218[231]
TITLE REFERENCE | 19.218[231]
THIS OF THE TRANSCHIPS | 19.218[231]
THE TRANSCHIPS | 19.21
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24

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32 ; Search time 8.24352 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

Title: US-10-092-750-38
Perfect score: 187
Sequence: 1 MAVIINELSQRDSCGPLKISLANKILVYGNLFSSFTP 37

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	polyprotein - infe	probable exported	hypothetical prote		hypothetical prote	hypothetical prote	щ	TonB-dependent rec	conserved hypothet		hypothetical prote		cell surface prote	hypothetical prote	penicillin-binding	proline-rich prote	probable S-recepto	core antigen - hep	hypothetical prote	conserved hypothet	u	general secretion	te-like	unc-22	급	74	Н	hypothetical prote	П
SUMMARIES	ΩI	T00327	AH0446	S40938	H90538	H84862	875372	E81792	D81215	B98021	G90091	E90284	T51044	T17456	T42328	G89935	S1674B	T14471	S53221	T26612	E81706	AI1225	AG0099	T41568	A88852	S57242	T27935	7	90	S59384
	DB	7	N	7	N	N	N	N	~	7	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	7	N	N	~
	Length	3085	1307	619	1128	504	137	703	703	307	670	247	461	1402	599	691	449	857	183	471	826	188	318	834	6831	6839	7160	518		1435
dю	당성	31.6	30.5	29.4	29.1	28.9	28.6	28.6	28.6	28.3	28.3	27.8	27.0	27.0	26.7	26.7	26.5	26.5	26.2	26.2	26.2	25.9	25.9	25.9	25.9	25.9	25.9	25.7	ů.	25.7
	Score	59	57	55		54	ω,	53.5	ë.		53		50.5		20	20	49.5	•	49		49			8	œ	φ.			4.8	4.
	Result No.	:	73	e	4	Ŋ	Q	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps

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Query Match 30.5%; Score 57; DB 2; Length 1307; Best Local Similarity 50.0%; Pred. No. 11; Matches 13; Conservative 3; Mismatches 10; Indels

hypothetical prote	chalcone synthase	hypothetical prote	hypothetical prote	ribulose-bisphosph	ribulose-bisphosph	genome polyprotein	hypothetical prote	hypothetical prote	MHC class II OLA-D	hypothetical prote	glutamate-5-semial	gamma-glutamylphos	gamma-glutamylphos	hypothetical prote
AC1579	T10742	H90094	B72314	139557	139559	GNNY1B	S34617	T16468	I47094	T27198	RDECER	D85513	F90662	F90497
20	10	~	N	N	N	Н	~	~	N	~	-	N	N	7
188	390	446	471	485	486	2157	141	146	232	237	417	417	417	478
25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1
47.5	47.5	47.5	47.5	47.5	47.5	47.5	47	47	47	47	47	47	47	47
30	3 6	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
•	propriotein - infectious flacherie virus C;Species: infectious flacherie virus C;Species: Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
	C;ACCESBION: 17032/ R;Isawa, H.; Asano, S.; Sahara, K.; Ilzuka, T.; Bando, H. Arch. Virol. 143, 127-143, 1998 A;Title: Analysis of genetic information of an insect picorna-like virus, infectious flac
	ke) viruses. A, Reference number: Z14139; MUID:98166871; PMID:9505971 3.20cesion: m01377
	A,Status: Langered from GB/EMBL/DDBJ A,Molecule type: genomic RNA A,Residues: 1-3085 <1SA>
	A,Cross-references: UNIPROT:O70710; EMBL:AB000906; NID:g3025414; PIDN:BAA25371.1; PID:g3(C,Keywords: polyprotein
	Query Match 31.6%; Score 59; DB 2; Length 3085; Best Local Similarity 34.1%; Pred. No. 14; Matches 15; Conservative 8; Mismatches 9; Indels 12; Gaps 1;
	Qy 3 VIINELSQR
	Db 205 iSLNELTERYIVIANGVLTSGDTRGQVKFSLDLPAAIYGNLDSS 248
	RESULT 2
	probable exported protein YPO3670 [imported] - Yersinia pestis (strain CO92)
	C;Species: versinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
****	C,Accession: AH0446 R.Parkhill, J.: Wren. B.W.: Thomson. N.R.: Titball. R.W.: Holden. M.T.G.: Prentice. M.B.:
	deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F.; M. Ducharford V. Simmands M. Skelton, T. Stevens V. Whitehead S. Barrall I.
••	Nature 413, 523-527, 2001
	Affitie: Genome sequence of Yershila pestis, the causalive agent of plague. A,Reference number: AB0001; MUID:21470413; PMID:11586360
	A,Accession: AH0446 A,Status: preliminary
	A,Molecule type: DNA A,Residues: 1-1307 <kur></kur>
	A;Cross-references: UNIPROT:Q8ZAW2; GB:AL590842; FIDN:CAC93140.1; FID:g15981592; G5FDB:G: C;Genetics: * Acceleration
	Ajeme: 17030.0 C;Superfamily: Escherichia coli hypothetical protein yhdP
	Query Match 30.5%; Score 57; DB 2; Length 1307;

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Gaps

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R.Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.I. Mol. Microbiol. 22, 175-191, 1996
Mol. Microbiol. 22, 175-191, 1996
A.Fitle: Organizational characteristics and information content of an archaeal genome: 18 A;Reference number: S73076; WUID:97055432; PMID:8899719
A;Accession: S75372
                                                                               A;Cross-references: UNIPROT:Q9ZW78; GB:AE002093; NID:g3763926; PIDN:AAC64306.1; GSPDB:GNC
C;Genetics:
A;Gene: At2g43170
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cjaccession: B81792
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Title: Complete DNa sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID:2022556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .cross-references: UNIPROT.09JRC7; GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85405; Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable TonB-dependent receptor protein NMA2193 [imported] - Neisseria meningitidis (strace) - Species: Neisseria meningitidis
C.Species: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P95944; EMBL:Y08257; NID:g1707772; PID:e283873; PID:g1707777 A;Experimental source: strain P2 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996 C;Genetics: A,Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein c04005 - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S75372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53.5; DB 2; Length 137; Pred. No. 3; Mismatches 11; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
                                                                                                                                                                                                                          Length 504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VIINELSQR-----DSCGPLKISLNNKILVYGN 30
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Pred. No. 17;
4; Mismatches
                                                                                                                                                                                                                       Score 54; DB
Pred. No. 10;
                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                          266 QRTQSGPVTLQGNNNVM--GDMFSQATP 291
                                                                                                                                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                                                                                                 10 ORDSCGPLKISLNNKILVYGNLFSSFTP
                                                                                                                                                                                                                          28.9%;
39.3%;
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Best Local Similarity 38.9%;
Matches 14; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.0°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                     Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-137 <SEN>
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                                                                    A, Residues: 1-504 <STO>
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                     A, Status: preliminary A, Molecule type: DNA
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A; Accession: H84862
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90538
R;Chanbaud, I:; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MuID:21267165; PMID:11353084
A;Accession: H90538
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-1128 <KUR>
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Hyd862
Hyd862
Hyd862
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Hyd862
Hyd90thetical protein At2g43170 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84862
E;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Residues: 1-1128 «KUR»
A,Cross-references: UNIPROT:Q98QZ4; GB:AL445566; PID:g14089629; PIDN:CAC13389.1; GSPDB:G
A,Experimental source: strain UAB CTIP
C,Gene: MyPU 2160
A,Genetic code: SGC3
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A;Tile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein MYPU 2160 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C,Species: Mycoplasma pulmonis
C,Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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                                                                                                                                                                      hypothetical protein ZK632.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40938
R;Berks, M.
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Pred. No. 9.3;
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4; Mismatches
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Pred. No. 21
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43.5%;
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1 Similarity 47.1%;
16; Conservative (
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                                                                                                                                                                                                                                                                                                   Submitted to the EMBL Data Lister of the EMBL Data Lister of the EMBL Data Lister of A; Reference number: $40933 A; Accession: $40938 A; Molecule type: DNA
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Best Local Similarity
Matches 16; Conserv
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us-10-092-750-38.rpr

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-670 cDOJ>
A;Cestuses: 1-670 cDOS=references: UNIPROT:Q98RT4; GB:AF165818; NID:g13794489; PIDN:AAK39864.1; GSPDB:G)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: E90284
A;Atatus: preliminary
A;Atatus: preliminary
A;Residues: 1-247 <KUR>
A;Cross-references: UNIPROT:Q97YM8; GB:AE006641; NID:gl3814496; PIDN:AAK41532,1; GSPDB:GP
C;Genetics:
A;Gene: SSO1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T51044
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 < SCH>
A;Residues: 1-461 < SCH>
A;Cross-references: UNIPROT:09P3J7; EMBL:AL389900; GSPDB:GN00116; NCSP:B15120.140
A;Experimental source: BAC clone B15120; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related to spore coat protein SP96 precursor [imported] - Neurospora crassa NiAlternate names: protein B15120.140
C.Species: Neurospora crassa
C.Species: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SSO1294 [imported] - Sulfolobus solfataricus
C,Species: Sulfolobus solfataricus
C,Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                              Gaps
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  A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: G90091
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                                                                                                                                                                                                                                                                                                                 Length 670;
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73
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Pred. No. 20;
7; Mismatches
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Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 IINELSQRDSCGPLKISLNNKILVYGNL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.8%;
                                                                                                                                                                                                                                                                                                                 28.3%;
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Best Local Similarity 36.6
Matches 15; Conservative
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Best Local Similarity 35.77
Matches 10; Conservative
                                                                                                                                                                                        A Gene: orf670
A,Map position: 1
A,Genome: nucleomorph
C,Keywords: nucleomorph
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Best Local Similarity
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                                                            RESULT 8
D81215
TonB-dependent receptor, probable NMB0293 [imported] - Neisseria meningitidis (strain MC c)species: Neisseria meningitidis
C;Species: Neisseria meningitidis
R;Tettelin, H.; Sauders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
R;Tettelin, H.; Sauders, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Tettele: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Reference: number: A81000; MUID:20175755; PMID:10710307
A;Residues: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9JRC5; GB:AE002386; GB:AE002098; NID:g7225512; PIDN:AAF4074
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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d90091
hypochetical protein orf670 [imported] - Guillardia theta nucleomorph
c;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G90091
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.;
Nature 410, 1091-1096, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53.5; DB 2; Length 7
Pred. No. 17;
4; Mismatches 15; Indels
AKVVEDKENPDRVG---IHLNNTSNVTGNLFFRYTP 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            590 AKVVEDKENPDRVG---IHLNNTSNVTGNLFFRYTP 622
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Best Local Similarity 38.9%;
Matches 14; Conservative
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A;Residues: 1-691 «KUR»
A;Cross-references: UNIPROT:Q99TU2; GB:BA000018; PID:g13701350; PIDN:BAB42644.1; GSPDB:GR
C;Genetics:
A;Gene: pbp3
                                                                                                                                                                                                                                                                                                                                                                                    26.7%; Score 50; DB 2; Length 691; ilarity 34.6%; Pred. No. 55; Conservative 7; Mismatches 10; Indels
A; Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 10, 2004, 13:40:46 Job time : 9.24352 secs
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Best Local Similarity
Matches 9; Conserv
                                                                                      A;Status: preliminary A;Molecule type: DNA
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AyTitle: A novel Dictyostellum cell surface protein important for both cell adhesion and AyReference number: Z18798; MUID:98359946; PMID:9693138

AyAccession: T17456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1402 cdIN>
A;Residues: 1-1402 cdIN>
A;Cross-references: UNIPROT:096668; EMBL:AF102575; NID:g4063398; PID:g4063399; PIDN:AAC9
A;Experimental source: strain Ax2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - phage SPP1
C;Species: phage SPP1
C;Species: phage SPP1
C;Date: 03-Dec-1999 #sequence_revision, 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision, 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1997
R;Alonso, J.C.; buder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Alien The complete nucleotide sequence and functional organization of Bacillus subtil
A;Reference number: Z22137; WUID:98094274; PMID:9434185
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                                                                                                                                                                                                                                                                                                                                                       cell surface protein DTPA - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
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A;Residues: 1-599 <ALO>
A;Cross-references: UNIPROT:048488; EMBL:X97918; PIDN:CAA66535.1
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                Indels
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                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.0%; Score 50.5; DB 2; Best Local Similarity 37.1%; Pred. No. 1e+02; Matches 13; Conservative 7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AVIINELSQRDSCGPLKISLNNKILVYGNLFSSFT 36
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Pred. No. 47;
5; Mismatches 1:
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                                                                                                                                        6 NELSQRD---SCGPLKISLNNKILVYGNLFSS 34
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Best Local Similarity 33.3%;
Matches 10; Conservative
                Conservative
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                    12;
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Q8ep29 oceanobacil

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C6m621 corynebacte
Caf19856 corynebac
C4r4b9 ashbya goss
A74r4b ashbya goss
A72z29 xenopus lae
Q9dhr3 yaba-like d
Q867b0 can1s famil
Q86594 dictyostell
Q864ku8 brassica ol
Q84ku8 brassica ol
Q84ku8 brassica ol
Q84ky9 brassica ol
Q84ky9 brassica ol
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MEDLINE=98166871; PubMed=9505971;
ISAWA H., Asano S., Sahara K., Ilzuka T., Bando H.;
"Analysis of genetic information of an insect picorna-like virus, infectious flacherie virus of silkworm: evidence for evolutionary relationships among insect, mammalian and plant picorna(-like)
                                                                                                                                                                                                                                                                                                                                                                                                 DNA stage; Iflavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.6%; Score 59; DB 2; Length 3085; 34.1%; Pred. No. 80; :ive 8; Mismatches 9; Indels
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                      Polyprotein.
Infectious flacherie virus.
Viruses; ssRNA positive-strand viruses, no
NCBI_TaxID=12742;
                                                                                                                                                                                                                           ALIGNMENTS
             OBNRA1
O6M621
CAF19856
Q74ZH9
AASS4713
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Q867B0
Q867G4
Q9PYW1
Q84KU8
Q84KY9
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01-OCT-2000 (TrEMBLrel. 15, C. 01-OCT-2000 (TrEMBLrel. 15, L. 01-MAR-2004 (TrEMBLrel. 26, L. F16B3.28 protein.
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   000000000000000
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Best Local Similarity 34.1
Matches 15; Conservative
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PRELIMINARY;
Polyprotein
SEQUENCE
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P34652 caenorhabdi
Q66d3 yarrowia li
Q84x06 brassica ol
Q83x23 pseudomonas
Q92x78 arabidopsis
P95944 aufolobus
Q91pk2 neisseria m
Q91pk1 neisseria m
Q91pk3 neisseria m
Q91pk3 neisseria m
Q91pk3 neisseria m
Q91pc7 neisseria m
Q91c7 neisseria m
Q91c7 neisseria m
Q91c7 neisseria m
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Q86k14 dictyosteli
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OBzaw2 yersinia pe
Aas64021 yersinia
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guillardia
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xestia c-ni
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Q8dpf1
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Q97ym8
Q7tsf9
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      1825181 seqs, 575374646 residues
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09M877
086K14
08D1P4
08ZAW2
AAS64021
POLG HRV16
CALX CAEEL
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0898C24
0898C24
0898C24
0898C24
089C24
094A14
094A11
094PK1
099FKC7
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Maximum Match 1008
Listing first 45 summaries
                                                                      protein search, using sw model
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Q97YM8
Q7TSF9
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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187
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Match
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Maximum DB
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Gaps

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SEQUENCE FROM N.A.
STRAIN-KIMS, / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21470413; PubMeda1586360; DOI=10.1038/35097083; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., Baker S., Babhan D., Bentley S.D., Brooks K., Cerdeno-Tarzaga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quall M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Wedner 413:523-527(2001):
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Complete proteome.

SEQUENCE 1307 AA, 14414 MW; F2C5A282B066CE54 CRC64;
                                                                                                                                                                                   Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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01-MAR-2002 (TTENBLrel. 20, Created)
01-MAR-2002 (TTENBLrel. 20, Last sequence update)
01-0CT-2004 (TTENBLrel. 28, Last annotation update)
Putative exported protein.
OrderedLocusNames=YP3876, YP03670;
                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.5%; Score 57; DB Best Local Similarity 50.0%; Pred. No. 50; Matches 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184.4601.4611(2002).
EMBL, AE013619; AAM83789.1; -.
HYDOCHELICAL DECEDIN.
SEQUENCE 1063 AA; 116550 MW; BO5D377F05
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      Created)
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01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein y0195, OrderedLocusNames=y0195;
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Q8ZAW2
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                                                                                                                                                                                                             LIN X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,
A Ronning C.M., Koo, H., Fujii C.Y., Utterback T.R., Barnstead M.B.,
Bowman C.L., White O., Nierman W.C., Traser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, ACO21840; AAF32472.1;
InterPro; IPR002885; PPR.
R InterPro; IPR002885; PPR.
R InterPro; IPR00215; Prot_inh_serpin.
R Pfam; PP03140; DUF247, 1.
R Pfam; PP03140; DUF247, 1.
R TIGRPAMS; TIGR00756; PPR; 8.
R TIGRPAMS; TIGR00756; PPR; 7.
R TIGRPAMS; TIGR00756; PPR; 7.
R SEQUENCE 1077 AA; 121922 MW; 4ABFIFE09A8DC7AB CRC64;
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                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-VAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Gpl38.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 660 AA; 73846 MW; 3E8341398E7A6CB9 CRC64;
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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28.6%; Pred. No. 43;
:ive 9; Mismatches
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48.3%; Pred. No. 30;
tive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22092622; PubMed=12097910;
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Best Local 6
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PRT; 1063 AA

PRELIMINARY;

Q8D1P4 Q8D1P4;

RESULT 4 Q8D1P4

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Structure 1:51-68(1993).
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           THERE EXECTED BY AND BY
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-2004 (Rel. 45, Last amnotation update)
01-OCT-2004 (Rel. 45, Last amnotation update)
Genome polyprotein [Contains: Coat protein VP4 (PlA); Coat protein VP2 (PlB); Coat protein VP2 (PlB); Coat protein VP4 (PlD); Core protein P2A; Core protein P2C; Core protein P2A; Genome-linked protein VPG (PBB); Protein P2C; Core protein P3A; Genome-linked protein VPG (PBB); Protein NPG (PBB); Protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
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MEDLINE=95250310; PubMed=7732663;
Lee W.M., Mang W., Rueckert R.R.;
"Complete sequence of the RNA genome of human rhinovirus 16, a
clinically useful common cold virus belonging to the ICAM-1 receptor
                                                                                       Gaps
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MEDLINE=94348864; PubMed=7915182;
Olivelra M.A., Zhao R., Lee W.M., Kremer M.J., Minor I.,
Rueckert R.R., Diana G.D., Pevear D.C., Dutko F.J., McKinlay M.A.,
Rossmann M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=91001 / Blovar Mediaevalis;
STRAIN=91001 / Blovar Mediaevalis;
STRAIN=91001 / Blovar Mediaevalis;
STRAIN=91001 / Blovar Mediaevalis;
SONG Y., Tong Z., Wang J., Han Y., Kang J., Li S., Guo Z.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
Yang R.,
Submitted (ARR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB017142; AAS64021.1;
SEQUENCE 1307 AA, 144414 MW, F2C5A282B066CE54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
NCBI_TaxID=632,
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       DB 2; Length 1307;
62;
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                                                                                   10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-WAR-2004 (TrEMBLrel. 27, Created)
24-WAR-2004 (TrEMBLrel. 27, Last sequence update)
04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                               3; Mismatches
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       Score 57;
Pred. No. 6
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                                                                                                                                                           7 ELSQRDSCGPLKISLNNKILVYGNLF 32
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Virus Genes 9:177-181(1995).
       Query Match
Best Local Similarity 50.0%;
Matches 13; Conservative
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POLG HRV16
ID POLG HRV16
AC Q82122;
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AAS64021;
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                                                                       ProDom; PD001274; Pico_P2B; 1.
SMART; SM0382; AAA, 1.
3D-structure; Coat protein; Core protein; Hydrolase; Lipoprotein;
Myristate; Polyprotein; RNA-directed RNA polymerase; Thiol protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
                                                                                                                                                                                                                                                                                                                                                                                               {RNA}(N): The virus capsid is composed of 60 icosahedral units, each of which is composed of one copy each of proteins VP1, VP2, VP3, and VP4.
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X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 2-853, AND REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coat protein VP4.
Coat protein VP2.
Coat protein VP3.
Coat protein VP1.
Core protein P2A.
Core protein P2B.
Core protein P2C.
Core protein P3A.
Genome-linked protein VPG.
Picornain 3C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L24917; AAA69862.1; -.
PDB; LAYM; X-ray; 1=569-853; 2=70-330; 3=331-568.
PDB; LAYN; X-ray; 1=569-853; 2=70-330; 3=331-568.
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InterPro; IPR00189; Peptidase C3.
InterPro; IPR00189; Peptidase C3.
InterPro; IPR001809; PeptiCallcin.
InterPro; IPR001809; Pept Callcin.
InterPro; IPR001809; Pept Callcin.
InterPro; IPR001818; PicC-PlA.
InterPro; IPR001857; PicC-PlA.
InterPro; IPR001676; RNv.
InterPro; IPR001676; RNv.
InterPro; IPR001095; RNA_Pol DS_PS.
InterPro; IPR001205; RNA_Pol PSD.
InterPro; IPR001895; Viral_cap_coat.
InterPro; IPR0018975; Viral_cap_coat.
InterPro; IPR008975; Viral_cap_coat.
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Pfam; PP00947; Pico_P2A; 1.
Pfam; PP00047; Pico_P2B; 1.
Pfam; PF00073; Rhv; 3.
Pfam; PP006060; Rhv; 4ep_RNA_pol; 1.
Pfam; PP00910; RNA_helicase; 1.
PRINTS; PR00918; CALICVIRUSNS.
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PD001306; Pico_P2A; 1.
PD001274; Pico_P2B; 1.
                                                           MEDLINE=97238938; PubMed=9083115;
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SEQUENCE FROM N.A.

STRAIN=Bristol N2;

XX MEDLINE=94150718; Pubmed=7906398;

Wilson R., Jainscough R., Anderson K., Baynes C., Berks M.,

Milson R., Darton J., Connell M., Copsey T., Cooper J., Coulson A.,

Bonfield J., Burton J., Cannell M., Copsey T., Cooper J., Craston M.,

Bonfield J., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,

Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownken R.,

Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,

Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,

Nohldman P.,

T. 2. Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                              30.2%; Score 56.5; DB 1; Length 2153; 41.0%; Pred. No. 1.38+02; 7ative 8; Mismatches 6; Indels 9
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nes 16; Conservative
  CAEEL
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Matches 16;
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CALX CAEEL
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AC P34652;
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   RNA-directed RNA polymerase. N-myristoyl glycine (by host).
            N-myristoyl glycine (b
Protease (Potential).
Protease (Potential).
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIJEE-222866392; PubMed=12399400;
SALO.INE-222866392; PubMed=12399400;
SALO.K., Nishio T., Kimura R., Kusaba M., Suzuki T., Hatakeyama K., Ockendon D.J., Satta Y.,
Cockendon D.J., Satta Y.,
"Coevolution of the S.locus genes SRK, SLG and SP11/SCR in Brassica cleracea and B. rapa "; Genetics 162:931-940(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 29.1%; Score 54.5; DB 2; Length 438; Local Similarity 40.6%; Pred. No. 45; Loss 13; Conservative 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                            SEQUENCE 1914 AA; 220365 MW; 1DE84B605332F9ED CRC64;
                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
5-locus receptor kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

29.4%; Score 55; DB 2; Best Local Similarity 46.9%; Pred. No. 1.8e+02; Matches 15; Conservative 5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 LSIXINTLSSRES---LKISSNRTLVSPGSIF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 INELSORDSCGPLKISLNNKIL--VYGNLFSS 34
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GO; GO:0004872; F:kinase activity; IEA.
GO; GO:0005872; F:receptor activity; IEA.
GO; GO:000529; F:sugar binding; IEA.
InterPro; IPR001480; B_lectin.
InterPro; IPR003609; Pan app.
InterPro; IPR003609; Pan app.
Ffam; PF00453; Blectin; 1.
Pfam; PF00454; S_locus_glycop.
Ffam; PF00554; S_locus_glycop.
FMART; SM00473; PAN AP.
PROSITE; PS50927; BULB LECTIN; 1.
PROSITE; PS50927; BULB LECTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                          Genoscope;
Submitted (JUL-2004) to the
EMBL; CR382129; CAG81624.1;
NON_TER
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                                 Nature 430:35-44(2004)
"Genome evolution in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 AA;
                                                                                                                SEQUENCE FROM N.A. STRAIN=CLIB99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinase; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3712;
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SEQUENCE
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Q98QZ4;
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Q98QZ4
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    SFREERS
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                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ORFNames=YALIOCO1411g;
Yarrowia lipolytica (Candida lipolytica).
Functi al (Sandida lipolytica).
Eukaryota; Fundi, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 619 Calnexin homolog. .) (Potential). 203 203 N-linked (GLGNAC. .) (Potential). 571 N-linked (GLGNAC. .) (Potential). 619 AA, 69207 MW, 08903CE519A75B88 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R INCACT, P34552; ---
R WOTMPEP, ZK632.6; CE00423.
R INTERPRO; IPRO1580; Calret calnex.
R INTERPRO; IPRO19985; Cona like lec_gl.
R INTERPRO; IPRO19985; Cona like lec_gl.
R Pfan; PF00262; Calreticulin; 1.
R PROSTE; PS00806; Calreticulin; 1.
R PROSITE; PS00803; CALRETICULIN 1; 1.
R PROSITE; PS00804; CALRETICULIN 1; 1.
R PROSITE; PS00805; CALRETICULIN 2; 1.
R PROSITE; PS00805; CALRETICULIN 3; 1.
R PROSITE; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.4%; Score 55; DB 1; Length 619;
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
reticulum (By similarity). SIMILARITY: Belongs to the calreticulin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1914 AA.
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                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 222181; CAA80183.1; -. PIR; 540938; 540938. HSSP; P18418; 1K9C.
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nes 10; Conservative
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Bukaryota, Varidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.

NCBL_TAXID=3702,
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Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
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Subunsley S.D., Jin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Romning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Koesema 2., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,
Banh J., Bowser L., Carrinci P., Dale J.M., Goldsmith A.D.
Hayashizaki Y., Ishida J., Jang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Falm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick P.
Tang C.C., Torlumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theelogis A., Ecker J.R.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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      Indels
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Town C.D., Kaul S.;
Submitted (FES-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004450; AAC64306.1; -.
PIR; H84862; H84862.
HYDOCHELICAL Protein.
SEQUENCE 504 AA; 52252 MW; 8B6E7FD3D6F100FB CRC64;
                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein At2943170.
Arabiatory
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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      Mismatches
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                                                                                               124 GALKVRFSNSVLKYGNOFMS 143
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ო
                                                             15 GPLKISLNNKILVYGNLFSS
      10; Conservative
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Best Local Similarity
Matches 11; Conserv
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      Matches
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Q94A14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                      STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Perris S., Barbe V., Samson D., Galisson Mosser I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
"The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mypulist; MYPU 2160; -. GO: 0004435; F:phosphoinositide phospholipase C activity; IEA. GO: 00:0004435; F:phosphoinositide phospholipase C activity; IEA. GO: 00:000629; P:lipid metabolism; IEA. InterPro; IPR001326; Lipoprotein_17. InterPro; IPR001711; PI_PLC_Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas fluorescens.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                              Mycoplasma pulmonis.
Bacteria<u>i Firmi</u>cutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF04200; Lipoprotein 17; 4.
PROSTIE; PS50008; PIPLC Y DOMAIN; 1.
Complete proteone; HypcChetical protein.
SEQUENCE 1128 AA, 127054 MW; 5605405000742EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45856 MW; ACD0DA8697A1CA8B CRC64;
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EMBL; AB088043; BACG5314.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005741; C:mitochondrial outer membrane; IEA.
GO; GO:0005288; F:porin activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR005318; OprD.
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein MYPU_2160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; DB 2;
1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 IINELSQRDSCGPLKISLNNKILVYGNLFSSFTP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 54.5; DB
; Pred. No. 1.2e+
4; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
EMBL; AL445563; CAC13389.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.1%;
                                                                                                                     OrderedLocusNames=MYPU_2160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 47.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H90538; H90538
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Best Local Similarity
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=2107;
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Query Match

Matches

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RESULT 12
083V23
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DT 01-JUN-10
DT 01-JUN-10
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINS=2133296; PubMed=11427726;

A Mayez M.J. Chan-Weiher C.C.-Y. Clausen I.G., Curtis B.A.,

A Mayez M.J. Chan-Weiher C.C.-Y. Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

A Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

A The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RThe complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RThe complete Sci. U.S.A. 98:7835-7840(2001).

B FNBL; ARGO651; ARK40472.1; -.

DR FIRE; ARGO651; ARK40472.1; -.

SW Complete protecome; Hypothetical protein.

SW Complete protecome; Hypothetical protein.
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Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
L Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; AT050457; AAK91411;
R EMBL; BT002247; AAK91411;
R EMBL; BT002247; AAK91411;
R EMBL; BT002247; AAK912288.1;
R HSSP; O88339; IEDU.
R InterPro; IPR008943; Pl bind N.
R Pfam; PF01417; ENTH; 1.
R Pfam; PF01417; ENTH; 1.
R PROSITE; PS50942; ENTH; 1.
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U-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Orf C04005 protein (Hypothetical protein SSO0117).
Orf C04005 protein (Hypothetical protein SSO0117).
Sulfolobus solfatarious
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.9%; Score 54; DB 2; Length 895; 39.3%; Pred. No. 1.1e+02; ive 6; Mismatches 9; Indels
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40.0%; Pred. No. 18;
ive 3; Mismatches
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STRAIN=P2;
MEDLINE=97055432; PubMed=8899719;
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Best Local Similarity 39.3
Matches 11; Conservative
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NCBI_TaxID=2287;
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P95944;
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Sequence 19247, A Sequence 14, Appl Sequence 14, Appl Sequence 20111, A Sequence 45764, A Sequence 24981, A Sequence 22, Appl Sequence 26528, A Sequence 26528, A Sequence 2057, A Sequence 2057, A Sequence 30524, A Sequence 39270, A Sequence 32728, A Sequence 32728
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Sequence 968, App
Sequence 24429, A
Sequence 279, App
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191.991 Million cell updates/sec
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-109-790-045-14
US-10-222-578-14
US-10-222-578-14
US-09-252-991A-20111
US-09-270-767-45426
US-09-269-731-8
US-09-269-731-8
US-09-269-731-8
US-09-269-731-8
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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8 45.2 157 4 US-09-258-991A-16827 Sequence 8 45.2 178 4 US-09-252-991A-16827 Sequence 8 45.2 181 4 US-09-252-991A-16827 Sequence 8 45.2 181 4 US-09-232-308A-2 Sequence 8 45.2 233 4 US-09-107-532A-6778 Sequence 8 45.2 276 4 US-09-107-532A-6778 Sequence 8 45.2 294 4 US-09-492-985-2 Sequence 8 45.2 294 4 US-09-249-86-2 Sequence 8 45.2 294 4 US-09-270-76-1181 Sequence 8 45.2 323 4 US-09-76-1821 Sequence 8 45.2 323 4 US-09-76-1821 Sequence 8 45.2 324 US-09-76-1821 Sequence 8 45.2 364 US-09-76-1821 Sequence <th>21632, A</th> <th>16827, A</th> <th>43724, A</th> <th>2, Appli</th> <th>4778, Ap</th> <th>6776, Ap</th> <th>7430, Ap</th> <th>2, Appli</th> <th>41531, A</th> <th>2, Appli</th> <th>1821, Ap</th> <th></th> <th>1821, Ap</th> <th>172, App</th> <th>172, App</th> <th>783, App</th> <th>783, App</th> <th>172, App</th>	21632, A	16827, A	43724, A	2, Appli	4778, Ap	6776, Ap	7430, Ap	2, Appli	41531, A	2, Appli	1821, Ap		1821, Ap	172, App	172, App	783, App	783, App	172, App
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ALIGNMENTS

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Sequence 19247, Application US/09248796A
Sequence 19247, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
THE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VS-09-045-14

VS-09-045-14

VS-09-045-14

Sequence 14, Application US/09790045

PETERT NO. 6495210

GENERAL INFORMATION:

APPLICANT: Hasebe, Akira

APPLICANT: Hasebe, Akira

APPLICANT: Hasebe, Akira

APPLICANT: Horita, Mitsuo

TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia Solanacearum

APPLICANT:

APPLICANT: Horita, Mitsuo

TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia Solanacearum

PETER REFERENCE: NAN-106US

CURRENT APPLICATION NUMBER: US/09/790,045

CURRENT FILING DATE: 201-02-21

NUMBER OF EQ ID NOS: 14

SOFTWARE: Patentin version 3.0

LENGTH: 274

LENGTH: 274

TYPE: PRT

CORGANISM: Ralstonia solanacearum
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Pred. No. 38;
4; Mismatches 3; Indels
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KKSKRNPANLTPP 16
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12 KRKRKNPSTTTPP 24
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Best Local Similarity 46.2
Matches 6; Conservative
RESULT 1
US-09-248-796A-19247
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US-09-790-045-14

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, ORGANISM: Drosophila melanogaster US-09-270-767-45426
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US-09-252-991A-20111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
13 LARKTKRYPSDLT 25
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Best Local Similarity 58.3
Matches 7; Conservative
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40 ESRRSPAHLRPP 51
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                                                                           RESULT 5
US-09-252-991A-20111
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LENGTH: 427
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                                                                                                                                                                                                                                              Sequence 14, Application US/10222577

Sequence 14, Application US/10222577

Petent No. 6538125

GENERAL INFORMATION

APPLICANT: Hasebe, Akira

APPLICANT: Horita, Miteuo

TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia

TITLE OF INVENTION: Solanacearum

TITLE OF INVENTION Solanacearum

TITLE APPLICATION NUMBER: US/10/222,577

CURRENT APPLICATION NUMBER: US/09/790,045

PRICR APPLICATION NUMBER: US/09/790,045

PRICR PLING DATE: 2001-02-21

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.0
                                                                               Gaps
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APPLICANT: Hasebe, Akira
APPLICANT: Hasebe, Akira
APPLICANT: Tsuchiya, Kenichi
Batent No. 6570007
TITLE OF INVENTION: Solanacearum
FILE REFERENCE: NANP10808
CURRENT APPLICATION NUMBER: US/10/222,578
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 18/09/790,045
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                                      Score 42; DB 4; Length 274; Pred. No. 32; 4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/10222578; Patent No. 6570007; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Ralstonia solanacearum
US-10-222-577-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OKGANISM: Ralstonia solanacearum
US-10-222-578-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
                                        50.0%;
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13 LARKTKRYPSDLT 25
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                                                                                                                      2 LAKKSKRNPANLT 14
                                        Query Match
Best Local Similarity 61.5
Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                RESULT 3
US-10-222-577-14
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LENGTH: 274
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Sequence 20111, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: MAKE J. Rubenfield et al.
APPLICANT: MAKE J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
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US-09-270-767-45426
; Sequence 45426, Application US/09270767
; Sequence 45426, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT HOMBUTGER et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
; CURRENT PILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 391;
46;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OS/269,731
FILING DATE: CASSIFICATION DATA:
FRIDASIFICATION DATA:
APPLICATION NUMBER: WO FR97/01768
FILING DATE: OC-CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 96 12204
FILING DATE: O'-OCT-1996
ATTORNEY-APPLICATION DATA:
FILING DATE: O'-OCT-1996
ATTORNEY-AGENT INFORMATION:
FILING DATE: O'-OCT-1996
ATTORNEY-AGENT INFORMATION:
FILING DATE: O'-OCT-1966
ATTORNEY-AGENT INFORMATION:
FILEPHONE: (703) 412-1155
TELEPHONE: (703) 412-1161
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 annino acids
TYPE: amino acid
TYPE: amino acid
TYPE: APPR: protein
US-09-269-731-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.8%; Score 41; DB 3; Length 545; S0.0%; Pred. No. 95; tive 4; Mismatches 4; Indels
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Pred. No. 12;
1; Mismatches 3; Indels
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US-09-896-720-22

j Sequence 22, Application US/09896720

j Patent No. 675067

GENERAL INFORMATION:

APPLICANT: SONG, WEN-YUAN

J APPLICANT: PI, LI-YA

TITLE OF INVENTION: UBIQUITIN LIGASE

FILE REFERENCE: 5853-173

CURRENT APPLICATION NUMBER: US/09/896,720

CURRENT FILING DATE: 2001-09-24

PRIOR FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTION OF 22

LENGTH: 50

TYPE: PRT

TYPE: PRT

COGANISM: OTYZE SETIVE
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Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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US-09-252-991A-24981

US-09-252-991A-24981

Sequence 24981, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABSTUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
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US-09-269-731-8

i Sequence 8, Application US/09269731

j Sequence 8, Application US/09269731

j Patent No. 6333165

dENERAL INFORMATION:
    APPLICANT: BARBEYON, Tristan
    APPLICANT: POTIN, Philippe
    APPLICANT: POTIN, Philippe
    APPLICANT: RICHARD, Christophe
    APPLICANT: RICHARD, Christophe
    APPLICANT: WIN, Jean-Claude
    APPLICANT: KLOAREG, Bernard
    TITLE OF INVENTION: use for producing enzymes for the biodegradation of
    TITLE OF INVENTION: carrageenans
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
    STREET: 612 Crystal Square 4; 1745 Jefferson Davis
    STATE: VIRGINIA
    COUNTRY: U.S.A.
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Pred, No. 1.3e+02;
1; Mismatches 2; Indels
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48.8%; Score 41; DB 4; Length 400;
Best Local Similarity 46.7%; Pred. No. 69;
Matches 7; Conservative 4; Mismatches 4; Indels
                                                                                  ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-24981
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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127 LARRRQRDPAGAQPP 141
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Best Local Similarity 70.0%;
Matches 7; Conservative
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              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45764
LENGTH: 1059
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456 RRKPQNLTPP 465
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RESULT 11
US-09-248-796A-26528
; Sequence 56528, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; APPLICANT: Keith Weinstock al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
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gequence 30524, Application US/09252991A

| Sequence 30524, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICATION:
| APPLICATION:
| TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TILE REPRENCE: 107196.136
| CURRENT PILING DATE: 1999-02-18
| PRIOR PILING DATE: 1999-02-18
| PRIOR PILING DATE: 1998-02-18
| PRIOR PILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| SEQ ID NO 30524
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,110
FILING DATE: Filed Herewith
CLASSIFCATION DATA:
APPLICATION NUMBER: US/09/829,110
FILING APPLICATION DATA:
APPLICATION NUMBER: BY TOWN WARE: BILLINGS, LUCY J.
REGISTRATTON NUMBER: PF-0259 US
REGISTRATTON NUMBER: PF-0259 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-85-0555
TELEPAX: LUCY J.
SEQUENCE CHRACAFERISTICS:
LENGTH: 159 amino acids
TYPE: Amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.6%; Score 40; DB 4; Best Local Similarity 50.0%; Pred. No. 42; Matches 7; Conservative 4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 2;
Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/09896720
; Patent No. 6750057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
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81 ACRSRRNPGSPSPP 94
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158909
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino constraint STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-252-991A-30524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Pseudor
US-09-252-991A-30524
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Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC--007

FILE REPERENCE: GTC--007

CURRENT PPLICATION NUMBER: US/09/134,001C

CURRENT PPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

NUMBER: OF SEQ ID NOS: 5674

SEQ ID NO 5657

LENGTH: 112
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Sequence 1, Application US/08829110

Patent No. 5892890

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Hillman, Jennifer L.

APPLICANT: GOIL, SULYA K.

TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN

TITLE OF INVENTION: SIGNALING

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
  TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196-1132
CURRENT PILING DATE: 10999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PLICATION NUMBER: US 60/074,725
PRIOR PLICATION NUMBER: US 60/096,409
PRIOR PLICATION NUMBER: US 60/096,409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 26528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Porter Drive CITY: Palo Alto STREE: CA Alto COUNTY: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Staphylococcus epidermidis US-09-134-001C-5057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AKKSKRNPANLTPP 16
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                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26528
                                                                                                                                                                                                                                                                                                                                                                                                                        3 AKKSKRNPANLTP 15
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ZIP: 94304
COMPUTER READABLE FORM:
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## APPLICANT: SCNG, WEN-YUAN

## APPLICANT: SCNG, WEN-YUAN

## APPLICANTON: UBIQUITIN LIGASE

FILE REFERENCE: 5853-173

## CURRENT APPLICATION NUMBER: US/09/896,720

CURRENT FILING DATE: 2001-09-29

## PRIOR APPLICATION NUMBER: 60/215,049

## PRIOR PLING DATE: 2000-06-29

## PRIOR FILING DATE: 2000-06-29

## PR
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Search completed: November 10, 2004, 13:44:10 Job time: 6.52677 secs

:| || |||| 354 NKPNPTTLTPP 364

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 10, 2004, 16:36:12; Search time 17.1883 Seconds (without alignments) 328.807 Million cell updates/sec			
5:36:12 ; Se (with 328.8		vo	s. c
), 2004, 1	750-39	VPANLTPP 1	, Gapext
November 10	US-10-092-750-39	84 1 GLAKKSKRNPANLTPP 16	BLOSUM62 Gapop 10.0 , Gapext 0.5
Run on:		Periect score: Sequence:	Scoring table: BLOSUM62 Gapop 10

Total number of hits satisfying chosen parameters:

1566620 segs, 353225886 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

| cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/PCT TIME PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/USO9_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/USO0_NEW_PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	39, Ap	3417, Ap	211273,	228508	64638, A	250313	211116	191510	168814	253454,	335386	306150,	353683,
Description	Sequence 39, Appl	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	US-10-092-750-39	US-10-264-049-3417	JS-10-425-115-211273	US-10-425-115-228508	-10-425-114-64638	-10-425-115-250313	US-10-424-599-211116	US-10-425-115-191510	-10-424-599-168814	US-10-425-115-253454	JS-10-425-115-335386	JS-10-425-115-306150	US-10-425-115-353683
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% Query Match	100.0	73.8	57.1	56.0	56.0	56.0	54.8	54.8	53.0	52.4	52.4	52.4	51.8
Score	84	62	48	47	47	47	46	46	44.5	44	44	44	43.5
Result No.	н	~	m	4	ഗ	y	7	80	6	10	11	12	13

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37-963-16 25-115-27 25-115-21 25-115-21 25-115-22 26-115-22 26-115-2 27-114-2 27-115-2 28-115-2 25-115-2 25-115-2 25-115-2 25-115-2 25-115-2 25-115-2 25-115-2 25-115-2 25-115-2	US-10-408-765A-64 US-10-405-115-212 US-10-404-929-273 US-09-988-201-8 US-09-988-202-8 US-09-988-202-8 US-10-431-963-197 US-09-895-720-22 US-10-425-115-366 US-10-425-115-366 US-10-425-115-36
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ALIGNMENTS

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Gaps
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US-10-092-750-39

US-10-092-750-39

Sequence 39, Application US/10092750

Publication US/0030032157A1

GENERAL INFORMATION

APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia

APPLICANT: Wright, Martin C.

ITILE OF INVENTION: POlypeptides Interactive with BCL-X1

FILE REPRENCE: 50036/05002

CURRENT FILING DATE: 2002-03-07

PRIOR PILING DATE: 2001-03-08

NUMBER: OF SEQ ID NOS: 253

SOFTWARE: FESTESEQ for Windows Version 4.0

SEQ ID NO 39

LENGTH: 16

"WORD ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 84; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-39
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; Sequence 3417, Application US/10264049; Publication No. US20040005579A1; GENERAL INFORMATION: RESULT 2 US-10-264-049-3417

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US=10-425-114-64638
; Sequence 64638, Application US/10425114
; Sequence 64638, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Enou, Yihua
; APPLICANT: Soreen, Seven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE SFERENCE: 38-21(531313)
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF, SEQ ID NOS: 73128
; SEQ ID NO 64638
; SEQ ID NO 64638
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exvalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: And K.
APPLICANT: AND FIGURE ACID Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 256313
LENGTH: 446
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Pred. No. 20;
0; Mismatches 2; Indels
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US-10-425-114-64638
                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_139992C.1.pep
US-10-425-115-228508
  FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 228508
LENGTH: 143
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Best Local Similarity 81.0.
9; Conservative
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                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
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; Sequence 211273, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION: Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION UNMSER: US/10/425,115
; CURRENT APPLICATION NUMSER: US/10/425,115
; CURRENT FILING DATE: 2003-64-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 211273
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-3417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 228508, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nuclaic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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## APPLICANT: Birse et al.

## TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
#FILE REFERENCE: PAl33P1
CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT FILING DATE: 2002-10-04

PRIOR PILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: Patentin Ver. 3.1

LENGTH: 23
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US-10-425-115-211273
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73.8%; Score 62; DB:
Best Local Similarity 75.0%; Pred. No. 0.01:
Matches 12; Conservative 0; Mismatches
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75 LFKEKKKNPGFLTPP 89
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE LOCATION: (6)
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-10-425-115-253454
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US-10-425-115-253454
US-10-425-115-253454
US-10-425-115
US-10-425
                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.4%; Score 44; DB 17; Length 109; Best Local Similarity 52.9%; Pred. No. 44; Matches 9; Conservative 3; Mismatches 3; Indels
    Length 538,
                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Clone ID: PAT_MRT3847_123454C.1.pep
US-10-424-599-168814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_162731C.1.pep
US-10-425-115-253454
Query Match
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
FRATURE:
LOCATION: (1)..(170)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GLAKKSKRNPANLTPP 16
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                                                                                                                                                                                                                                           358 ISTRKSRNPALLTPP 372
                                                                                                                                                                                       2 LAKKSKRNPANLTPP 16
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
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US-10-424-599-211116
US-10-424-599-211116
Sequence 211116, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rowalt David K
APPLICANT: Cav Yihua
APPLICANT: Cav Yougwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 211116
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 101510, Application US/10425115
| Sequence 101510, Application US/10425115
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: La Rovalic, David K.
| APPLICANT: Cao, Yongwei |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants
| TITLE REFERENCE: 38-21 (53222)
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 369326
| SEQ ID NO 191510
| LENTH: 538
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                                                                                                                                                                                                                        Query Match 56.0%; Score 47; DB 17; Length 446; Best Local Similarity 81.8%; Pred. No. 63; Matches 9; Conservative 0; Mismatches 2; Indels
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US-10-424-599-211116
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106236C.1.pep
US-10-425-115-191510
                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_159873C.1.pep
US-10-425-115-250313
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Pred. No. 37;
3; Mismatches 3.
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LOCATION: (1)..(184)
PERTION: unsure at all Xaa locations
PEATURE:
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Best Local Similarity 53.8%;
Matches 7; Conservative
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24 KKKKKNPKKISPP 36
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              ORGANISM: Zea mays FEATURE:
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1 GLAKKS--KRNPANLTP 15

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SEQ ID NO 353683
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(Sequence 335386, Application US/10425115

(Sequence 335386, Application US/10425115

(SENDRAL INFORMATION:
(SENDRAL INFORMATION:
(APPLICANT: La Rosa, Thomas J.)
(APPLICANT: La Rosa, Thomas J.)
(APPLICANT: Cao, Yongwei C.)
(AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20040214272A1

Publication No. US20040214272A1

Publication No. US20040214272A1

Publication No. US20040214272A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: 191arts

TITLE OF INVENTION: 1010428

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 366150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 17; Length 160;
Pred. No. 65;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_68982C.1.pep
US-10-425-115-335386
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US-10-425-115-306150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(160)
OTHER INFORMATION: unsure at all Xaa locations
66 GIKKKTGFKKNPVNCTP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KKSKRNPANLTPP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 KKKKKNPPNPFPP 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
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US-10-425-115-306150
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RESULT 13

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Sequence 169759, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Caro, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF SEQ INVENTION: VINNER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
EDROTH: 66
                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Expansion and M.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FURENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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Pred. No. 38;
1; Mismatches 4; Indels
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US-10-437-963-169759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 43.5; DB 17;
56.2%; Pred. No. 39;
tive 4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Clone ID: MRT4577_85733C.1.pep US-10-425-115-353683
Sequence 353683, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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; Sequence 279854, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GLAKKSKRNPANLTPP 16
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7 GIPRKSQR-PLSLTPP 21
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Best Local Similarity 61...
Best Local 8; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-437-963-169759
```

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## APPLICANT: Kovalic, David K.

### APPLICANT: Zhou, Yihua

### APPLICANT: Zhou, Yihua

### APPLICANT: Zhou, Yihua

### APPLICANT: Cao, Yongwel

### TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

### TITLE OF INVENTION: Plants

### TITLE OF INVENTION: Plants

### CURRENT APPLICATION NUMBER: US/10/425,115

### CURRENT FILING DATE: 2003-04-28

### CURRENT FILING DATE: 2003-04-28

### TYPE: PRT

### ORGANISM: Zea mays

### TYPE: PRT

### OTHER INFORMATION: Clone ID: MRT4577_186806C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%; Pred. No. 77; Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLAKKSKRNPANLTPP 16
|:||| |:
|18 GVAKKKKKKKKKTPP 133
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Search completed: November 11, 2004, 01:28:21 Job time: 18.2383 secs

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OM protein - protein search, using sw model

Run on:

November 10, 2004, 12:29:32; Search time 3.56477 Seconds (without alignments) 431.857 Million cell updates/sec

US-10-092-750-39 84 1 GLAKKSKRNPANLTPP 16 Title: Perfect score:

Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	pice	hypothetical prote	arginine-tRNA liga	arginyl-tRNA synth	neural zinc finger		-eu	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	two-component syst	ocin AP41]	1				dTMP kinase (EC 2.	hypothetical prote	ABC transporter, A	beta-lytic metallo	hypothetical prote		molybdopterin oxid	ABC transporter-li	exiT protein - Myc	genome polyprotein
ΙD	S67131	S70704	10	LO.	F81075	T14124	S67044	G02133	T26823	D86193	T45926	H69363	B82545	830271	833442	S33441	E72622	A85063	A84971	AC3108	A98179	LYYXLY	AG2008	410	C75525	T47648	418	806188
DB	0.0																											
Length	306	409	4	Ľ	ഹ	2	726	268	569	280	281	265	629	777	843	1822	116	164	212	346	371	374	567	683	697	720	1122	N
* Query Match	0.5	50.0	0	0	0	0	σ	œ	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.6	٠	47.6	
Score	4.4			42	42	42	41.5	41	41	41	41	41	4.	41	41	41	40	40	40	40	40	40	40	40	40	40	4.0	40
Result No.	⊣ ¢	4 M	4	Ŋ	y	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps ;

Query Match
Best Local Similarity 66.7%; Pred. No. 79;
Matches 8; Conservative 2; Mismatches 2; Indels

hypothetical prote	hypothetical prote	FMRFamide-like pep	lysozyme (EC 3.2.1	hypothetical prote	glycoprotein gp63	hypothetical prote	probable salt-indu	probable arginyl-t	transcription fact	transcription fact	glycyl-tRNA synthe	hypothetical prote	hypothetical prote	F13B4.4 protein -	hypothetical prote
T50315	E75077	T26262	AD3322	T47760	VGBE63	E71677	D84778	T36252	539356	S61977	AB1257	T27402	\$57157	E86268	T52517
N	~	N	~	7	Н	~	N	~	~	~	~	~	0	N	~
780	118	184	277	298	350	415	497	586	644	676	688	969	707	786	929
47.0	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4
39.5	39	99	39	39	39	39	39	39	39	39	39	39	39	39	39
30	31	32	33	34	32	36	37			40	41	42	43	44	45

ALIGNMENTS

RESULT 1 S67131
hypothetical protein YOR238w - yeast (Saccharomyces cerevisiae) N.Alternate names: hypothetical protein O5237 C.Snedies: Sarcharomyces cerevisiae
C. Accession: S6713
R.Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; Dujon, B. submitted to the Protein Sequence Database, July 1996
A.Reference number: S67104 A.Accession: S67131
A; Molecule type: DNA A; Residues: 1-306 <boy></boy>
A,Cross-references: UNIPROT: Q08634; EMBL: Z75146; NID: g1420544; PID: g1420545; GSPDB: GN0001 A,Experimental source: strain S288C
A;Gene: MIPS:YOR238w A;Gross-references: SGD:SC005764 A;Map position: 15R
52.48;
best Local Similarity 60.0%; Fred; NO. 13; Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2 LAKKSKRNPANLTPP 16
Db 253 LTKKRSRNPFNRTAP 267
RESULT 2
T31635
hypothetical protein YS7A10A.m - Caenorhabditis elegans C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000 C:Accession: T31635
R,Smye, R. submitted to the BMRT. Data Library. September 1999
A) Reference number: 221048
A;Accession: T31635 A;Status: preliminary; tranglated from GB/EMBL/DDBJ
A, Molecule type: DNA
A.Crosiduca: 1.11.7 T.1.7.7 A.Crosimences: EMBL:AL117195; PIDN:CAB55018.1; CESP:Y57A10A.m A.Experimental source: clone Y57A10A
 C,Genetics:
A;Gene: CESP:Y57A10A.m A;Introns: 106/3; 257/3; 286/1; 405/2; 452/2; 504/2; 687/2; 811/1; 945/2; 1045/3; 1121/3
 C;Superfamily: DNA-directed DNA polymerase, mitochondrial

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1 GLAKKSKRNPANLTPP

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arginine-tRNA ligase (EC 6.1.1.19) NMA1707 [imported] - Neisseria meningitidis (strain 27. 5) pecies: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-Nay-2000 #sequence_revision 05-Nay-2000 #text_change 09-Jul-2004
C;Accession: F81866
B;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MulD:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:09JTM7; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84938
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciacter of man-every meaguence_revision 31-Mar-2000 #text_change 09-Jul-2004
Ciaccession: Fallors
Ritetain, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arginyl-tRNA synthetase NMB1506 [imported] - Neisseria meningitidis (strain MC58 serogrou C;Species: Neisseria meningitidis (c;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:Q9JYM8; GB:AE002500; GB:AE002098; NID:g7226744; PIDN:AAF4186; A,Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neural zinc finger factor 3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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54;
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54;
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50.0%; Score 42; DB

Best Local Similarity 61.5%; Pred. No. 54;

Matches 8; Conservative 2; Mismatches
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Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: argS; NMA1707
C,Superfamily: arginine-tRNA ligase
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C,Superfamily: arginine-tRNA ligase
16
                                16 GTAVKMNRMPSSLSPP 31
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45 GAAKKAKQNPREL 57
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Matches 8; Conserv
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A:Molecule type: DNA
A;Residues: 1-572 <PAR>
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A;Molecule type: DNA
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F81866
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 16-Jul.1999 #sequence_revision 16-Jul.1999 #text_change 09-Jul-2004
C; Accession: T10652
R; Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro submitted to the Protein Sequence Database, June 1999
A; Reference number: Z16533
A; Accession: T10652
A; Molecule type: DNA
                                                                                                                                                                                                                                     Carbon catabolite repressor crel - fungus (Trichoderma harzianum)
N,Alternate names: glucose repressor crel
C;Species: Trichoderma harzianum
C;Species: Trichoderma harzianum
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: $770704; $73106
R;Ilmen, M.; Thrane, C.; Penttilae, M.
Mol. Gen. Genet. 251, 451-460, 1996
My;Thrane, C.; Penttilae, M.
A;Title: The glucose repressor gene crel of Trichoderma: isolation and expression of a synccession: $70704
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A;Experimental source: cultivar Columbia; BAC clone T5F17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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A,Gene: crel
C;Keywords: DNA binding; repressor; transcription regulation; zinc finger
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A;Map position: 4
A;Mtcons: 97/1: 243/3: 328/3
C;Superfamily: Arabidopsis thaliana hypothetical protein F17J16.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.0%; Score 42; DB 2; Length 419; Best Local Similarity 50.0%; Pred. No. 39; Matches 8; Conservative 3; Mismatches 5; Indels
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A;Residues: 1-268,'S',270-409 <ILW>
A;Residues: EMBL:X95369; NID:g1177688; PID:g1177689
A;Experimental source: strain T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Score 42; DB 2;
57.1%; Pred. No. 38;
tive 2; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-409 <ILM1>
A,Cross-references: UNIPROT:Q99005; EMBL:X95369
A,Experimental source: strain T3
A,Accession: S77920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: mRNA
Residues: 1-409 <ILM2>
Cross-references: EMBL: X95369
Experimental source: strain T3
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262 AKRSRPNPPNSTAP 275
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Best Local Similarity 57.1<sup>3</sup>
Matches 8; Conservative
                                                                :||||:|| | | 455 SKKSKKNPKNST 466
                                3 AKKSKRNPANLT 14
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A;Accession: S73106
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Cybechetical protein [imported] - Arabidopsis thaliana
Cybechetical protein [imported] - Arabidopsis thaliana
Cybeches: Arabidopsis thaliana (mouse-ear cress)
Cybeches: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cybecesion: D86193
Cybeches: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change;
Cybeches: Date: Dat
                                                           A;Residues: 1-268 <SCH>
A;Cross-references: UNIPROT:P53701; EMBL:U36787; NID:g1209634; PIDN:AAB19007.1; PID:g120:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9XXF3; EMBL:AL023838; PIDN:CAA19501.1; GSPDB:GN00022; CESP:)
A;Experimental source: clone Y43C5A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Y43C5A.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26823
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C,Superfamily: Arabidopsis thaliana hypothetical protein F5K20.160
                                                                                                                                                                                                                                                                                                                                                                                                  Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 2;
Pred. No. 36;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-269 <WIL>
                                                                                                                                                                                 A,Gene: GDB:HCCS; CCHL
A,Cross-references: GDB:636832; OMIM:300056
A,Map position: Xp22-Xp2-
C;Keywords: carbon-sulfur lyase; mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riwhite, S.
submitted to the EMBL Data Library, June 1998
A;Reference number: 220272
A;Accession: T26823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLAKKSKRN--PANLTPP 16
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                                                                                                                                                                                                                                                                                                                                                                                                       48.8%;
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A;Introns: 9/3; 47/2; 85/2; 227/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0 Matches 9; Conservative
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A,Molecule type: DNA
A,Residues: 1-280 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Gene: CESP: Y43C5A.5
                      A; Molecule type: mRNA
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Best Local S:
Matches 7
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National Pages (Saccharomyces Cerevisiae)

C; Species: Saccharomyces cerevisiae

R; Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winsc submitted to the Protein Sequence Database, July 1996

A; Rocession: S67044

A; Rocession: S67044

A; Rocession: S67044

A; Rocession: Scouse to the EMBL Data Library, August 1995

A; Experimental source: strain S288C

R; Pringle, J.R.

Submitted to the EMBL Data Library, August 1995

A; Reference number: S59360

A; Accession: S9360

A; Acc
C; Accession: T14124

R; Yee, K.S.Y.; Yu, V.C.

R; Yee, K.S.Y.; Yu, V.C.

J; Si6-5374, 1998

A; Title: Isolation and characterization of a novel member of the neural zinc finger fact A; Accession: T14124

A; Accession: T14124

A; Residues: preliminary; translated from GB/EMBL/DDBU

A; Molecule type: mRNA

A; Mosicules: 1-1032 cyEE>

A; Mosicules: 1-1032 cyEE>

A; Accession: T14124

A; Mosicules: 1-1032 cyEE>

A; Mosicules: 1-1032 cyEE>

A; Mosicules: 1-1032 cyEE>

A; Mosicules: 1-1032 cyEE>

A; Cross-references: UNIPROT: Q9QX27; EMBL: AF031942; NID: g2914750; PID: g2914751; PIDN: AAC4
C; Genetics:
A; Mosicules: T2F-3

C; Function:
A; Description: confers repression on the basal activity of promoters containing the constituents by Description factor; zinc finger

C; Keywords: DNA binding; transcription factor; zinc finger
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Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
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Pred. No. 1e+02;
1; Mismatches 4; Indels
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G02133
holocytochrome-c synthase (EC 4.4.1.17) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #te>
C;Date: 22-Be-1996 #sequence_revision 06-Jun-1997 #te>
C;Accession: G02133
R;Schaefer, L.; Ballabio, A.; Zoghbi, H.Y.
Submitted to the EMBL Data Library, September 1995
A;Reference number: H00824
A;Accession: G02133
A;Status: preliminary; translated from GB/EMBL/DDBJ
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NFI1 protein - yeast (Saccharomyces cerevisiae)
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Best Local Similarity 61.5%;
Matches 8; Conservative
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A,Cross-references: UNIPROT: Q9PAH2; GB:AE004061; GB:AE003849; NID:g9107747; PIDN:AAF8534: A,Experimental source: strain 9a5c
A,Experimental source: strain 9a5c
B,Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrer, H.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J,D.; Junquaira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
J,D.; Junquaira, M.L.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A,Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunae, L.R.; Olivaira, M.A.; de Rosa Jr., V.E.; de Oliveira, R.C.; Palmieri, D.A.
RAdrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A,Authors: ad Silva, A.C.R.; da Silva, F.R.; da Silva, Jr., W.A.; da Silvaire,
A,Reference number: A59328
A,Contents: annotation
C;Genetics:
A,Genetics:
A,Genetics:
A,Genetics:
A,Genetics:
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pyocin AP41 large chain - Pseudomonas aeruginosa transposon ThAP41
C;Species: Pseudomonas aeruginosa
C;Species: Ososep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S30271; A47060; S27605
R;Sano, Y.; Kageyama, M.
Mol. Gen. Carrier (Genet. 237, 161-170, 1993
A;Title: A novel transposon-like structure carries the genes for pyocin AP41, a Pseudomor A;Reference number: S30271; MUID:93204890; PMID:8384291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S30271
A;Molecule type: DNA
A;Residues: 1-777 <SAN>
A;Cross-references: UNIPROT:Q51502; GB:D12705; NID:g216903; PIDN:BAA02196.1; PID:g216904
R;Sano, Y.
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Pred. No. 88;
3; Mismatches
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466 GLARRERANPENL 478
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                     A; Residues: 1-629 <SIM>
                                                                                                                                                                                                                        A;Status: preliminary A;Molecule type: DNA
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C,Species: Archaeoglobus fulgidus
C,Species: Archaeoglobus fulgidus
C,Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C,Accession: H69363
R,Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Welson, K.E.; Ketchum, K.A.; Dodson
R,Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Welson, K.E.; Ketchum, K.A.; Dodson
Glodek, A.J. Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Alauthors: Utterback, T.; Cctton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woses, C.R.; Venter, J.C.
A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A,Rcession: H69363
A,Reference number: A69250; MuID:98049343; PMID:9389475
A,Rocession: H69363
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Rosiques: 1-565 < KLE>
A,Rocession: H56363
A,Cross-references: UNIPROT:029350; GB:AE001041; GB:AE001782; NID:92689364; PIDN:AAB9034
                                                                                                                                                                                                                                                                                                                             hypothetical protein F5K20.160 - Arabidopsis thaliana (5Species: Arabidopsis thaliana (mouse-ear cress) (5Species: Arabidopsis thaliana (mouse-ear cress) (5Date: 04-Reb-2000 #sequence_revision 04-Reb-2000 #text_change 09-Jul-2004 (5,Datession: T4596 #sequence_revision 04-Reb-2000 #text_change 09-Jul-2004 R.Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, January 2000 A.Reference number: 223017 A.Reference number: 223017 A.Status: preliminary
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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A;Introns: 1947.
A;Note: FSK20.160
C;Superfamily: Arabidopsis thaliana hypothetical protein F5K20.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 2; Length 281; Pred. No. 38; 4; Mismatches 3; Indels
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Pred. No. 79;
2; Mismatches 4; Indels
      Length 280;
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:Q9M340; EMBL:AL132960
A,Experimental source: cultivar Columbia; BAC clone F5K20
      5
48.8%; Score 41; DB
46.7%; Pred. No. 38;
tive 4; Mismatches
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Best Local Similarity 50.0%;
Matches 7; Conservative
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tes 8; Conservative
                                                                                                                             2 LAKKSKRNPANLTPP 16
                                                                                                                                                                                          1 MASASKQNPSSSKPP 15
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                                                                Conservative
                                 Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-281 < MON>
      Query Match
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Gaps

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3; Indels

Length 629;

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J. Bacteriol. 175, 912-915, 1993
A;Title: The inherent DNase of pyocin AP41 causes breakdown of chromosomal DNA.
A;Reference number: A47060; MUID:93139066; PMID:8423163
A;Accession: A47060
B;Status: preliminary
A;Molecule type: protein
A;Rolecule: Cype: protein
C;Superfamily: pyocin AP41 large chain
C;Keywords: bacteriocin
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                       Length 777;
                                                                                                                                                                                                                                                       Score 41; DB 2; Length 777
Pred. No. 1.18+02;
Mismatches 4; Indels
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Job time : 4.56477 secs

us-10-092-750-39.rpr

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November 10, 2004, 12:27:34; Search time 19.5371 Seconds (without alignments) 471.205 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                               - protein search, using sw model
                                                                                            OM protein
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US-10-092-750-39 84 1 GLAKKSKRNPANLTPP 16 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	O8aw61 brachydanio	>	Q75cn1 ashbya goss	н	Q7vb38 prochloroco	Q6slc1 cochliobolu	Aar29905 cochliobo		Q86kc9 dictyosteli	Q6bnw6 debaryomyce		Aaf48000 drosophil	Q7z8p4 emericella	074n70 nanoarchaeu	Aar38927 nanoarcha	Q6z2d7 oryza sativ	Bad03518 oryza sat			neurospoi			Q7uz24 rhodopirell		Q31471 morone saxa	Q72rc0 leptospira	Q8f4f0 leptospira	Aas70414 leptospir	46	~	Q8xui9 ralstonia s
SUMMARIES		QI .	Q8AW61	Q6C2U3	Q75CN1	AAS51116	Q7VB38	Q6SLC1	AAR29905	Q08634	Q86KC9	Q6BNW6	Q9VZ30	AAF48000	Q7Z8P4	Q74N70	AAR38927	Q6Z2D7	BAD03518	Q759V2	AAS52091	Q7RZZ8	Q9L4V1	Q7Q3N3	Q7UZ24	031466	Q31471	Q72RC0	Q8F4F0	AAS70414	005546	9 FA 9	6INX8Ö
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Q88eg7 pseudomonas Q7q2t0 anopheles g	Q7pjj0 anopheles g Q9m0h3 arabidopsis	073mj4 treponema d Aas12031 treponema	Q9jtm7 neisseria m	Q9jym8 neisseria m	Q8ihr3 plasmodium	Q96py4 homo sapien	Q9qx27 rattus norv	Q9vw51 drosophila	Aaf49098 drosophil	Q95ve6 drosophila
Q88EG7 Q7Q2T0	Q7₽JJ0 Q9M0H3	Q73MJ4 AAS12031	SYR NEIMA	1 SYR_NEIMB	QBIHR3	Q96PY4	Q9QX27	Q9VW51	AAF49098	Q95VE6
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33 33 33	ა ა გ. გ.	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                  Vormer. (U.M.R. 2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) SI:BAC6CSE.1 (Novel protein similar to human procadherin 15 (PCDH15))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                            Name=BA7CSB.1;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
NCBI_TaxID=7955;
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                                                                                                                                                                                                                           SECUENCE FROM N.A.
Lloyd D.;
Submitrol (JUN-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 4 cadherin domains.
EMBL; ALS92062; CAD52120.1; --
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01-007-2004 (TrEMBLrel. 28, Last sequence update)
01-007-2004 (TrEMBLrel. 28, Last annotation update)
Similar to KLAOD161159 Kluyveromyces lactis IPF 4333.1.
ORFNames=YALI0F051269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              623
69282 MW; 70EC5E2D0F8CFC3A CRC64;
                                                                                                                                                                                                                                                                                                 HSSP; PISIT6; INCJ.
GO; GO:0016620; C:membrane; IEA.
GO; GO:0005509; P:calcium ion binding; IEA.
GO; GO:0007156; P:homophilic cell adhesion; IEA.
InterPro; IPR002126; Cadherin.
Pfam; PF00028; Cadherin, 4.
SPR00215; CADHERIN.
                            623 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 716 AA.
                            PRT;
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NON TER 623 623 MW; 70E SEQUENCE 623 AA; 69282 MW; 70E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 LTDPSKLNPLNVTPP 250
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Best Local Similarity 60.0
Matches 9; Conservative
                            PRELIMINARY;
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                            Q8AW61
RESULT 1
08AW61
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Conservative
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Query Match
Best Local Similarity
Matches 8; Conserv
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STRAIN=ATCC 10895;
PubMed=15001715;
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01-0CT-2003
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AAS51116;
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Q7VB38
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A Lafontaine I., de Montigny J., Marck C., Neuveglies C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye P., Fairhead C., Fairhead C., Farry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyer P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Mal., Muller H.,
Nicaud J.M., Nikolski M., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Micker P., Soudiet J.L.;
Micker P., Soudiet J.L.;
Micker P., Soudiet J.L.;
Micker P., Soudiet J.L.;
Micker 430:35-44(2004).
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NCBI_TaxID=33169;
                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
NCBI_TaxID=4952;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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Science 304:304-307(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.0%; Score 47; DB 2; Length 716; 66.7%; Pred. No. 45; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382132; CAG77826.1; -.
SEOUENCE 716 AA; 76068 MW; 614189D84C66C243 CRC64;
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InterPro; IPR001950; TIF_SUII.
Pfam; PF01253; SUII; 1.
TIGRFAMS; TIGR01159; DRPl; 1.
SEQUENCE 199 AA; 22543 NW; 02433AB5F7F94F9C CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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      Yarrowia lipolytica (Candida lipolytica).
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174 QTHRSPANLTPP 185
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STRAIN=ATCC 10895;
PubMed=15001715;
                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Name=ACL112C;
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Q75CN1;
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MEDLINE-222010154; PubMed=12917486;

MEDLINE-222010154; PubMed=12917486;

A Dufresne A., Salanoubar M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarcva K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R.;

"Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome."; a nearly minimal oxyphototrophic genome."; a nearly minimal oxyphototrophic genome."; EMBL; ABO17164; AAQ00306.1; -

EMBL; ABO17164; AAQ00306.1; -

EMBL; ACO17164; AACO306.1; -

R GO; GO:0016740; Firansferase activity; IEA.

R GO; GO:0016740; Firansferase activity; IEA.

R InterPro; IPR002656; Acyl_transf.
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                                                           Gaps
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EMBL, AR016886; AAS5116.1; -. SEQUENCE 199 AA; 22543 MW; 02433ABSF7F94F9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium
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  Length 199;
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                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Predicted membrane associated acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashbya gossypii (Yeast) (Eremothecium gossypii).
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57.1%; Pred. No. 17;
iive 1; Mismatches
  5
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Score 46; DB
Pred. No. 17;
                                                        Mismatches
                                                                                                                                                                                                                                                                                                          PRT;
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STRAIN=SARG / CCMP 1375 / SS120;
                                                                                                                                                                                                                                                                                                                         23-APR-2004 (TrEMBLrel. 27, Cr
23-APR-2004 (TrEMBLrel. 27, La.
23-APR-2004 (TrEMBLrel. 27, Lat.
ACL112CP.
  54.8%;
57.1%;
                                                                                                                                             ||| |: | |||
184 AKKKKTPTTTPP 197
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                                                                                                             3 AKKSKRNPANLTPP 16
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Best Local Similarity 5/...
Best Local 8; Conservative
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SARBA

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Q6SLC1; Q6SLC1; RESULT 6 Q6SLC1 ID Q6SL

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STRAIN=C4;
PubMad=14665450;
Callett N.L., Yoder O.C., Turgeon B.G.;
"Whole-genome analysis of two-component signal transduction genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Aecomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                            Cochliobolus heterostrophus (Drechslera maydis).
Bukaryota; Fugli, Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.6%; Score 45; DB 2; Length 1943; S0.0%; Pred. No. 3e+02; Live 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal pathogens.";
Eukaryotic cell 2:1151-1161(2003).
EMBL; AY45029; AAA29055.1; -
SEQUENCE 1943 AA; 212673 MW; 8F8485E22FFC3A45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] -
SEQUENCE FROM N.A.
BOyer ', Fairhead C., Gaillon L., Galisson F., Michaux (
Thierry A., Dujon B.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
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EMBL, Z75146; CAA99459.1; -.
PIR, S67131; S67131.
SGD, S0050764; CS338w.
GO, GO:0005737, C:cytcoplasm; IDA.
SEQUENCE 306 AA; 35591 MW; 6CA44EED5C9D7E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
S. Cerevistae Chromosome XV reading frame ORF YOR238w
ORFNames=YOR238W;
                                                                                                     02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Putative response regulator receiver RIMISp.
                                             PRT; 1943 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 AA.
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Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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                                             PRELIMINARY;
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                                             AAR29905
AAR29905;
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Q86KC9
ID Q86K
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PubMed=14665450;
Catlett N.L., Yoder O.C., Turgeon B.G.;
"Whole-genome analysis of two-component signal transduction genes in
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Eukaryotic Cell 2:1151-1161(2003).

Eukaryotic Cell 2:1151-1161(2003).

Eukaryotic Cell 2:1151-1161(2003).

EMBL, AN456029 ARA29050.1.

EMBL, AN456029 ARA29050.1.

EnterPro; IPR011009; Kinase like.

InterPro; IPR001009; Kinase like.

InterPro; IPR000019; Prot Kinase.

InterPro; IPR000019; Prot Kinase.

InterPro; IPR000199; Response reg.

InterPro; IPR001299; Ser_thr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001039; Response reg; 1.

R Pfam; PR00069; Prinase; 1.

R Pfam; PR00069; Prinase; 1.

R Probom; P0000019; Prot Kinase; 2.

Probom; P0000019; Prot Kinase; 2.

R RMART; SM00219; TyrK; 1.

R RMART; SM01219; TyrK; 1.

R RMART; SM0119; PROTEIN KINASE DOM; 1.

R ROSITE; PS00110; PROTEIN KINASE SEGULATORY; 1.

R ROSITE; PS00110; RESPONSE REGULATORY; 1.

R RPOSITE; PS00110; RESPONSE REGULATORY; 1.

R RPOSITE; PS00110; RESPONSE REGULATORY; 1.

R RPOSITE; PS00110; RESPONSE REGULATION; Sensory transduction; Serind/threconine-protein kinase; Transferase.

SEQUENCE 1943 AA; 212673 MW; 8F8485E22FFC3A45 CRC64;
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Eukaryota; Fungi, Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5016;
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                                                                                                                                                                                          Score 45; DB 2; Length 696;
Pred. No. 97;
0; Mismatches 4; Indels
InterPro, IPRO06025, Pept M Zn BS.
Pfam; PF01757, Acyl transf 3; 1
PROSITE: PS000142; ZINC PROTEASE; UNKNOWN 1.
Acyltransferase; Complete proteome; Transferase.
SEQUENCE 696 Aa; 79572 MW; 628FF962C9072747 CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Putative response regulator receiver RIMISp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1943 AA.
                                                                                                                                                                                              53.6%;
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                                                                                                                                                                                                                        Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                       1 GLAKKSKRNPANL 13
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Best Local Similarity 50.0
Matches 8; Conservative
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., Abjee M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blackasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Boispons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Johen F., Muller H.,

Kerrest A., Koszul R., Lemaire M., Lemaire M., Lemaire M., Machori P.,

Rorned J.M., Nikolski M., Oztas S., Ozfer-Kalogeropoulos O.,

Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,

Swennene D., Tekkale F., Wesolowki-Louvel M., Westhof E., Wirth B.,

Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

"Genome evolution in yeasts.",
                                                                                                                                                                                                                                                                                                                                                                   Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
0RFNames=DEHA0E194049;
0RFNames=DEHA0E194049;
0Reatyomyces hansenii (Yeast) (Torulaspora hansenii).
0Reatyota; Fungi; Ascomycota; Saccharomycetes;
0CGLaromycetales; Saccharomycetaceae; Debaryomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumgart C;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2003): -.
InterPro, IPR008615; FNIP.
Pfam, PF05725; FNIP.
Hypothetical protein.
SEQUENCE 453 AA, 51421 MW, 5C79A3D45C13E1CD CRC64;
                                                                                               Hypothetical protein.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI TaxID=44689;
(TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22092622; PubMed=12097910;
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LNEKSLKNPLNIYPP 119
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STRAIN=CBS767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                         01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=AX4;
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STRAIN=CBS767;

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REMEDINES-20196006; PubMed=10731132,

RADARS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADARS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADARS M.D., Evals S.E., Richards S., Ashburner M., Henderson S.N.,

Burnton G.G., Wortnam J.R., Yandell M.D., Zhang O., Chen L.X.,

RADARI J.F., Agbayani A., Darater E.G., Helt G., Nelson C.R., Gabor G.L.,

RADARI J.F., Bencs P.V., Berman B.P., Bhandari D., Belahakov S.,

Ballew R.M., Basu H., Bazenbar B.P., Bhandari D., Bolahakov S.,

RADARIS K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RADARS M. Cawley S., Dahlker C., Davenport L. B., Davies P.,

Boxtova D., Bocchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RADARDOR K., Downes M., Dugan-Rocha S., Pleischmann W.,

RADARDOR K., Downes M., Dugan-Rocha S., Pleischmann W.,

RADARDOR K., Downes M., Dagar N.S., Gelbart W.M., Glasser K.,

RADARDOR K., Downes M., Laura C., Ferriera S., Fleischmann W.,

RADARDOR K., Downes M., Howland T.J., Merl M.H., Ibegwam C.,

RADARDOR K., Howland T.J., Wei M.H., Ibegwam C.,

RADARDOR K., Howland T.J., Wei M.H., Ibegwam C.,

RADARDOR K., Howland T.J., Wei M.H., Degwam C.,

RADARDOR K., Moy M., Murphy B., Mocheod M.P., Mocheeson D.,

RADARDOR K., Moy M., Murphy B., Mocheod M.P., Mocheeson D.,

RADARDOR K., Now M., Murphy B., Murphy L., Murshy L., Murshy L.,

Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RADARDOR K., Pletter S., Venter E., Wang A.H., Wang X.,

Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

Radardor M., Pittmen G., Pan S., Pollard J., Wang X.,

Radardor M., Pittmen G., Staplecon M., Strong K., Sun B.,

Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

Radibs R., Pector C., Thrare R., Venter E., Wang A.H., Wang X.,

Walls S.M., Woodager M., Worley K.C., Wu D., Yang S., Zho J.,

Raber S., Sparding A.C., Staunders R.D., Scheeler F.,

Raber S., Sparding A.C., Staunders R., Wallessendor M., Schon S.,

Raber S., Sha
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SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                   Length 688;
                                                                                                                                  1; Indels
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382137; CAG88371.1; -.
SEQUENCE 688 AA; 77169 MW; 23B2BBBB3F07BBD71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           (TremBlrel. 13, Created)
(TremBlrel. 16, Last sequence update)
(TremBlrel. 26, Last annotation update)
                                                                                   / Match 52.4%; Score 44; DB 2; L
Local Similarity 66.7%; Pred. No. 1.4e+02;
nes 8; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                 PRT; 3539 AA.
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01-MAR-2001 (
01-MAR-2004 (
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REDILINE-20196006; PubMed=10731132;

RADAMS M.D. Celniker S.E., Holf R.A., Evens C.A., Gocayne J.D.,

RADAMS M.D. Celniker S.E., Holf R.A., Evens C.A., Gocayne J.D.,

RADAMS M.D. Celniker S.E., Holf R.A., Evens C.A., Gocayne J.D.,

RADAMS M.D. Celniker S.E., Holf R.A., Canage M., Henderson S.N.,

RADAMS M.D. Censter S.E., Addrews P. Pfeiffer B.D.,

RADAMS M.D. Canager Y.H., Blazej R.G., Change M., Pfeiffer B.D.,

RADAMS M.D. Canager Y.H., Blazej R.G., Change M., Pfeiffer B.D.,

RADAMS M. Basun A., Baxendale J., Bandari D., Boladakov S.,

RADAMS M. Benos P.V., Berman B.P., Bandari D., Boladakov S.,

RADAMS M. Cawley S., Dahlke C., Davenport L.B., Coher A., Chandra I.,

RADAMS M. Cawley S., Dahlke C., Davenport L.B., Coher S.M.,

RADAMS M. Cawley S., Dahlke C., Davenport L.B., Davies P.,

RADAMS M. Cawley S., Dahlke C., Davenport L.B., Coher M., Classer K.,

RADAMS M. Cawley S., Dahlke C., Davenport L.B., Davies P.,

RADAMS M. Cawley S., Dahlke C., Davenport L.B., Coher M., Classer K.,

RADAMS M. Cawley S., Dahlke C., Davenport L.B., Davies P.,

RADAMS M. J. Evangalista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RADAMS M., Gabriellan A.E., Garg N.S., Gelbart W.M., Classer K.,

RADAMS M., Gabriellan A.E., Garg N.S., Gelbart W., Mourch J.A.,

RADAMS M., Maryory D., Heiman T.J., Hernandez J.R., Houck J.,

RADAMS M., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,

RADAMS M., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,

RADAMS M., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,

RADAMS M., Mattei M. W., Musphy B., Murphy L., Murany D.M., Wang Y., Lin X.,

RADAMS M., Mattei M. W., Mohary K., Wang M., Maryory D.M., Wang M.,

RADAMS M., Massarman D.A., Weinscock G.M., Keissenbach J.,

RADAMS M., Modager, Worley K.C., Wu D., Yang S., Yan Q.A., Ye J.,

RADAMS M., Marsay M., Weinscock G.M., Weissenbach J.,

RADAMS M., Marsay M., Radams M., Zhou X., Zhu S., Zhu X., Smith H.O.,

RADAMS M., Massarman D.A., Weinscock G.M., Weissenbach J.,

RADAMS M., Massarman D.A., Weinscock J.C.,

RAD
               George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                               Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misra S., Crosby M.A., Mingall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.4%; Score 44; DB 2; Length 3539;
53.3%; Pred. No. 8.4e+02;
ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003485; AAF48000.3; -
PlyBase; PBgn0030266; CGIII12.
GO; GO:0005634; C:nucleic acid binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPRO0087; Znf C2H2.
Ffam; PF00096; zf-C2H2; 3.
SMART; SM00355; Znf C2H2; 5.
PROSITE; PS00028; ZINC_FINGER_C2H2 1; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2 2; 3.
SEQUENCE 3539 AA; 384995 MW; 0BD4A2997D18E0CI CRC64;
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; 0BD4A2997D18E0C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                 a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=22426070; PubMed=12537573;
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MEDLINE=22426069; PubMed=12537572;
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Best Local Similarity 53.30,
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MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Patel S., Peiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Raminker J.S., Pries E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22426069; PubMed=12537572;
Mistra B., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Amainker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J. Kusso S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Gaps

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Droscophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Athropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachygera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[1]

Created)
Last sequence update)
Last annotation update)

01-APR-2004 (TrEMBLrel. 27, 01-APR-2004 (TrEMBLrel. 27, 01-APR-2004 (TrEMBLrel. 27,

CG11122-PA.

PRT; 3539 AA.

PRELIMINARY;

AAF48000 AAF48000

1502 LSKKSSRKPSPVPPP 1516

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16

2 LAKKSKRNPANLTPP

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RESULT 14
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Bisendle M., Oberegger H., Zadra I., Haas H.;

"The siderophore system is essential for viability of Aspergillus

nidulans: functional analysis of two genes encoding 1-ornithine N 5-

monooxygenase (sidA) and a non-ribosomal peptide synthetase (sidC).";

Mol. Microbiol. 49:359-376(2003).

-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, Emericella.
                                                                                                                                                                                                                                                                                          Length 3539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2; Length 4793;
Pred. No. 1.2e+03;
2; Mismatches 4; Indels
                                                                                                                                                                         Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: AERO03485; AAF48000.3; -...
Flymanee: FBGN01030266; CG11122.
SEQUENCE 3539 AA; 384994 MW; 0BD4A2997D18E0C1 CRC64;
                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00697; DNA_LIGASE A1; UNKNOWN 1.
PS00012; PHOSPHOPANTETHEINE; UNKNOWN 1.
4793 AA; 525432 MW; DD4186E99190B601 CRC64;
                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                        Score 44; DB 2; 1
Pred. No. 8.4e+02;
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 4793 AA.
                                                                                                                                                                                                                                                                                                                             3; Mismatches
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GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0048037; F:cofactor binding; IEA.
GO; GO:008152; P:metabolism; IEA.
InterPro; IPR010071; AA adenyl dom.
InterPro; IPR000873; AMP-bind.
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InterPro; IPR000977; DNA 14gase.
InterPro; IPR006162; Ppantne_S.
InterPro; IPR006163; Pp bind_S.
Pfam; PP00501; AMP-binding; 3.
Pfam; PP00568; Condensation; 4.
Pfam; PP00550; PP-binding; 5.
TIGRPANS; TIGR0173; AA-adenyl-dom; PROSITE; PS50075; AMP_BINDING; 5.
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LSKKSSRKPSPVPPP 1516
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Best Local Similarity 53.3%;
Matches 8; Conservative
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                                                                                       Submitted (SEP-2002)
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Name=sidC;
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Best Local Similarity
Matches 9; Conserv
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                                            SEQUENCE FROM N.A.
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PROSITE; P
SEQUENCE
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Q728P4;
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                                                                                                                                                                                                                                                                                                               Waters E., Hohn M.J., Ahel I., Graham D.E., Adams M.D., Barnstead M., Beeson K.Y., Blbbs L., Bolanos R., Keller M., Kretz K., Lin X., Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M., Soell D., Stetter K.O., Short J.M., Noorderwier M., "The genome of Nanoarchaeum equitans: Insights into early archaeal evolution and derived parasitism."

Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988 (2003).

BMBL, ABO17199, ARR38927.1; -. Complete protecome.

Complete protecome.
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STRAINEXIMENTALY

MALE 22946215; PubMed=14566062;

MALE 22966215; PubMed=11. Graham D.E., Adams M.D., Barnstead M.,

Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,

Mathur E., Ni J., Podar M., Richardson T., Sitton G.G., Simon M.,

Soell D., Stetter S., Short J.M., Noorderwier M.; extenter S.

The genome of Nanoarcheuw equitans: insights into early archaeal

evolution and derived parasitism.";

Proc. Natl. Acad. Sci U.S.A. 100:12984-12988(2003).

EMBL; ABO17199; AAR38927.1.

SEQUENCE 167 AA; 20126 MW; CCB6FD3DEOEA7483 CRC64;
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                                                                   Last sequence update)
Last annotation update)
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(TremBlrel. 27, Last sequence update)
(TremBlrel. 27, Last annotation update)
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red. No. 45;
Mismatches 4
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Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 4
  167 AA.
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Pred. No.
                                                                                                                                                                                  Archaea; Nanoarchaeota; Nanoarchaeum
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Archaea; Nanoarchaeota; Nanoarchaeum
NCBI_TaxID=160232;
                                                Created)
PRT;
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MEDLINE=22946215; PubMed=14566062;
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                                           (TrEMBLrel. 27, (TrEMBLrel. 27, (TrEMBLrel. 27,
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                                                                                                                                      OrderedLocusNames=NEQ071;
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  PRELIMINARY;
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                                                                                                                                                              Nanoarchaeum equitans
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                       NCBI_TaxID=160232;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                     Q74N70;
  Q74N70
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AAR38927
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Search completed: November 10, 2004, 13:38:44

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2 LAKKSKRNPANLTPP 16

Job time : 22.5371 secs

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Nables dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 1 - western lowland gorilla mitochoncy NADH2 dehydrogenase (ubiquinone oxidoreductase chain 1 character names: NADH-ubiquinone oxidoreductase chain 1 character names: NADH-ubiquinone oxidoreductase chain 1 character names: NADH-ubiquinone oxidoreductase chain 1 character name of the fact of pacesion: A59153

R;Xu, X.; Arnason, U.
No.; Biol. Evol. 13, 691-698, 1996

A;Xteles. A complete sequence of the mitochondrial genome of the Western lowland gorilla. A;Reference number: 217269; MUID:96212991; PMID:8676744

A;Reference number: 217269; MUID:96212991; PMID:8676744

A;Reference number: DNA

A;Residues: Preliminary; nucleic acid sequence not shown; translation oc shown; translatect, A;Wolecule type: DNA

A;Residues: 1-318 < xUX>
A;Resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NADH2 dehydrogenas
                                                                                       November 10, 2004, 12:29:32; Search time 6.90674 Seconds (without alignments) 431.857 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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1 ANLLLLMVPILIAMAFLMLTERKILGYIOPR 31
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                                                                                                                                                                                                                                                                 283416 segs, 96216763 residues
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No.
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C;Genetics:

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Gaps

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4;

Pred. No. 9.4e-08;

76.78;

23; Conservative

Best Local Similarity Matches 23; Conserv

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C;Accession: T11363
R;Xu, X.; Gullberg, A.; Arnason, U.
R;Xu, X.; Gullberg, A.; Arnason, U.
J. Mol. Evol. 43, 438-465, 1996
A;Title: The complete mitochondrial (mtDNA) of the donkey and mtDNA comparisons among for A;Reference number: Z17265; MUID:97032591; PMID:8875857
A;Accession: T11363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Moseiduse: 1-318 < XXXX-
A;Moseiduse: 1-318 < XXXX-
A;Moseiduse: 1-318 < XXXX-
A;Cross-references: UNIRROT: P92475; EMBL: X97337; NID: g1805746; PIDN: CAA66014.1; PID: g1806
A;Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: mitochondrion
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t)
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - horse mitochondrion C; Species: mitochondrion Equus caballus (domestic horse) (c; Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C; Accession: T11857 R; Xu, X.; Arnason, U. Gene 148, 357-362, 1994 A; Arnason, U. Gene 148, 357-362, 1994 A; Arnason, U. Gene 148, 357-362, MUD:95047450; PMID:7958969 A; Reference number: Z17369; MUD:95047450; PMID:7958969
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C.Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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A;Molecule type: DNA
A;Residues: 1-318 <XUX>
A;Cross-references: UNIPROT: P48652; EMBL: X79547; NID: G577571; PID: G577572; PIDN: CAA56079.
C;Genetics:
A;Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                         NADEZ dehydrogenase (ubiquinone) (EC 1.6.5:3) chain 1 - donkey mitochondrion C;Species: mitochondrion Equus asinus (donkey)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 106; DB 2; Length 318;
Pred. No. 3.4e-07;
6; Mismatches 3; Indels
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                                                                   2 NLLLLMVPILIAMAFLMLTERKILGYIQPR 31
                                                                                                                   2 NILTLLVPILIAMAFLTLVERKILGYMQLR 31
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70.0%;
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Matches 21; Conservative
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T11857
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T11247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: T11833
R;Arnason, U.; Gullberg, A.; Xu, X.
Hereditas 14, 185-189, 1996
A;Title: A complete mitochondrial DNA molecule of the white-handed gibbon, Hylobates lax
A;Reference number: 217353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genetic code: SGC1
A;Note: NADH1
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A,Genetic code: SGCI
A,Start codon: ATT
C,Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                               A;Genome: mitochondrion
A;Genetic code: SGCI
C;Superfamily: NAPH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
T11833
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - common gibbon mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: mitochondrion Hylobates lar (common gibbon, white-handed gibbon)
.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                     Gaps
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;Cross-references: UNIPROT:Q96126; EMBL:X99256; PIDN:CAA67628.1
;Experimental source: isolate Ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 117; DB 2; Length 318;
Pred. No. 1e-08;
2; Mismatches 3; Indels
                                                                                                                                                                                                                          Length 318;
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                                                                                                                                                                                                                                                                                                 1; Indels
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Pred. No. 1.2e-10;
2; Mismatches 1;
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A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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Best Local Similarity 90.3%;
Matches 28; Conservative
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l Similarity 83.3%;
25; Conservative
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome: mitochondrion
Genetic code: SGC1
Note: NADH1
A; Gene: NADH1
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - greater Indian rhinoceros mitochc s/species: mitochondrion Rhinoceros unicornis (greater Indian rhinoceros) (C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T11247
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Gaps

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A;Cross-references: U-318 CANUD-
A;Cross-references: UNIPROT: P03887; GB:J01394; NID:g336430; PIDN:AAB59268.1; PID:g336431;
B;Yagi, T.; Hatefi, Y.
Biol. Chem: 263, 16150-16155, 1988
A;Title: Identification of the dicyclohexylcarbodiimide-binding subunit of NADH-ubiquinor
A;Reference number: A31910; MUID:89034077; PMID:3141400
A;Recession: A31910
A;Residues: 1-15 cYAG>
C;Genetics: 1-15 cYAG>
A;Genetics: A1500
A;Genetic code: SGCI
C;Guperfamily: NADB: quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-ty
C;Keywords: blocked amino end; membrane-associated complex; mitochondrion; NAD; oxidative
F;1/Modified site: N-formylmethionine #status experimental
A;Genome: mitochondrion
A;Genetic code: SGC4
A;Genetic code: SGC4
C;Supert codon: SGC4
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t)
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; C
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A,Status: nucleic acid sequence not shown; translation not shown; not compared with conce
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A;Note: submitted to GenBank/EMBL/DDBJ December, 1994
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ASB888
ASB864
ASB864
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C;Species: mitochondrion Ornithorhynchus anatinus (duckbill platypus mitochondrion C;Species: mitochondrion Ornithorhynchus anatinus (duckbill platypus)
C;Species: 4-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: ASB888
R;Janke, A.; Gemmell, N.J.; Feldmaier-Fuchs, G.; von Haeseler, A.; Paabo, S.
A;Jitle: The mitochondrial genome of a monotreme--the platypus (Ornithorhynchus anatinus A;Reference number: A58888; MUID:97077300; PMID:8919867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MADEZ dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - bovine mitochondrion NADH2 dehydrogenase (ubiquinone) 29K chain; NADH-ubiquinone oxido N;Alternate names: NADH dehydrogenase (ubiquinone) 29K chain; NADH-ubiquinone oxido C;Species: mitochondrion Bos primigenius taurus (cattle)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Date: 18-Aug-1982 #sequence_revision A:R.; Eperon, I.C.; Sanger, F.; Young, J.; Mol. Biol. 156, 683-717, 1982
A;Reference number: A00152; MUID:83010260; PMID:7120390
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                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                          Score 104; DB 2;
Pred. No. 6.2e-07;
5; Mismatches 4;
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Best Local Similarity 70.0%;
Matches 21; Conservative
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A, Genome: mitochondrion
A, Genetic code: SGC1
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C;Species: mitochondrion Apis mellifera (honeybee)

C;Date: 15-Uul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Uul-2004

C;Accession: 552972

R;Crozier, R.H.; Crozier, Y.C.

R;Crozier, R.H.; Crozier, Y.C.

A;Title: The mitochondrial genome of the honeybee Apis mellifera: complete sequence and A;Reference number: 552960; MUD:93114603; PMID:8417993

A;Accession: 552972

A;Accession: 552972

A;Residues: 1-305 <CRO

A;Residues: 1-305 <CRO

A;Residues: 1-305 <CRO

C;Genetics:
                                                                                                     A; Reference number: Z17256; MUID:97051708; PMID:8896369
A; Accession: T11247
A; Status: preliminary; translated from GB/EWBL/DDBJ
A; Molecule type: DNA
A; Residuae: 1-318 < XUX.>
A; Residuae: 1-318 < XUX.>
A; Residuae: 1-318 < XUX.>
A; Cross-references: UNIPROT:096189; EMBL:X97336; NID:g1666193; PIDN:CAA66001.1; PID:g166
A; Experimental source: kidney
A; Generics:
A; Generics:
A; Generic code: SGC1
C; Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                         sequence of the greater indian rhinocerus, Rhind
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   R;Xu, X.; Janke, A.; Arnason, U.
Mol. Biol. Evol. 13, 1167-1173, 1996
A;Title: The complete mitochondrial DNA
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Best Local Similarity 66.7%;
Matches 20; Conservative
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A;Cross-references: UNIPROT:079874; EMBL:AF034253; NID:g4958951; PID:g4958952; PIDN:AAD34. R;Urbing, B.M. submitted to the EMBL Data Library, February 1999 ** A;Description: The complete mitochondrial DNA sequence of the pig (Sus scrofa). A;Reference number: Z17370 ** A;Accession: T11870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - African clawed frog mitochondrior N)Alternate names: NADH-ubiquinone oxidoreductase chain 1 - Species: mitochondrion Xenopus laevis (African clawed frog) (2,5pecies: mitochondrion Xenopus laevis (African clawed frog) (2,5pecies: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 09-Jul-2004 (2,5cession: A00411 R;Roe, B.A.; Ma, D.P.; Wilson, R.K.; Wong, J.F.H. B;Roe, B.A.; Ma, D.P.; Wilson, R.K.; Wong, J.F.H. A;Hitle: The complete nucleotide sequence of the Xenopus laevis mitochondrial genome. A;Reference number: A00155; MUD:85261388; PMID:4019494
                                                                                                                                                          P.C.; Mao, S.J.T.; Hue
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A,Genetic code: SGC1
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-ty
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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A,Gentico cote: SGC1
C,Superfamily: NADH:guinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t)
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; C
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A;Residues: 1-323 <ROE>
A;Cross-references: UNIPROT:P03890; GB:M10217; GB:X01600; GB:X01601; GB:X02890; NID:93437
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A,Molecule type: DNA
A,Residues: 1-55, F', 57-63, A, 65-77, A', 79-318 <URS>
A,Cross-references: EMBL:AJ002189; PIDN:CAA05229.1
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Pred. No. 2.3e-06;
5; Mismatches 5;
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63.3%; Pred. No. 2.3e-06;
iive 7; Mismatches 4;
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Best Local Similarity
Matches 19; Conserv
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C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P92659; EMBL:Y10524; NID:91850861; PIDN:CAA71536.1; PID:9185
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - North American opossum mitochond (Species: mitochondrion Didelphis virginiana, Didelphis marsupialis virginiana (North A C.)Date: O'-May-1995 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004 (C.)Accession: 847870, 842810 (C.)Accession: 847870, 842810 (C.)Accession: 137, 243-256, 1994 (C.)Accession: A.; Feldmaier-Fuchs, G.; Thomas, W.K.; von Haeseler, A.; Paeaebo, S. A.; Fille: The marsupial mitochondrial genome and the evolution of placental mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S47870
A;Molecule type: DNA
A;Residues: 1-318 <UAN>
A;Cross-references: UNIFROT:P41304; EMBL:Z29573; NID:g452251; PIDN:CAA82677.1; PID:g5555
C;Genetics:
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A,Gene: mitochondrion
A,Genetic ede: SGGI
C,Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C,Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Nibriz dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - wallaroo mitochondrion C;Species: mitochondrion Macropus robustus (wallaroo, euro)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: Til-189 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Jule C; Macropus C; Macropus C; Macropus C; Macropus robustus)
A;Reference number: Z17271; MuID:97188458; PMID:9037043
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                                                                                            Query Match 70.3%; Score 104; DB 2; Length 318; Best Local Similarity 66.7%; Pred. No. 6.4e-07; Matches 20; Conservative 7; Mismatches 3; Indels
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Pred. No. 2.3e-06;
7; Mismatches 4; Indels
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Score 103; DB 2; Pred. No. 8.8e-07; 5; Mismatches 4

Query Match
Best Local Similarity 70.0%;
Matches 21; Conservative

2 NILLLMVPILIAMAFIMLTERKILGYIQPR 31

à d

A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-318 <JAN>

A; Genome: mitochondrion

A; Note: NADH1 C; Superfamily: C; Keywords: men

Search completed: November 10, 2004, 13:40:35 Job time : 6.90674 secs

RESULT 14

NLLLLMVPILIAMAFLMLTERKILGYIQPR 31

à В

Query Match
Best Local Similarity 63.3%;
Matches 19; Conservative

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Mitochondrion.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butberia; Primates; Catarrhini; Hominidae; Homo.
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STRAIN-Signameanh10320HgC,
Starlkovskaya E.B., Sukernik R.I., Derbeneve O.A., Volodko N.V.,
Ruiz-Pesini E., Torroni A., Brown M.D., Lott M.T., Hosseini S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT37866,
01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Aac17866 homo sapi
O85kt1 homo sapien
O87kt2 homo sapien
O67002 homo sapien
O67002 homo sapien
O67002 homo sapien
O67712 homo sapien
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O7702 homo sapien
O7703 homo sapien
O7703 homo sapien
O7703 homo sapien
O8510 homo sapien
                                                                                                 November 10, 2004, 12:27:34; Search time 37.8532 Seconds (without alignments) 471.205 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                 1825181
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                      US-10-092-750-26
148.
1 ANLLLLMVPILIAMAFLMLTERKILGYIQPR 31
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AAT37866

CABATT1

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NUIM HUMAN

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CONTCD

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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Perfect score:
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Maximum DB
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No.
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318 AA

PRT;

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Cabrera V.M., Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C.;
Cabrera V.M., Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

--- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

--- SIMILARITY: Belongs to the complex I subunit 1 family.

R EMBL, AP381994; AAL54553.1; --

R OG 90:0005029; C:membrane; IEA.

R OG 00:0005739; C:mitochondrino; IEA.

R OG 00:0005139; C:mitochondrino; IEA.

R PROSITE; PS00667; COMPLEXI, NDI 1; 1.

R PROSITE; PS00667; COMPLEXI, NDI 1; 1.

R PROSITE; PS00667; Complexi, NDI 1; 1.

R PROSITE; PS00667; Complexi, NDI 2; 1.
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"Recent African origin of modern humans revealed by complete sequences
of hominoid mitochondrial DNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Pubmed=1294126; DOI=10.1093/molbev/msg230;
Pubmed=1294126; Doi=10.1093/molbev/msg230;
Moilanen J.S., Finnila S., Majamaa K.;
"Lineage-specific selection in human mtDNA: lack of polymorphisms in segment of MTNDS gene in haplogroup J.";
[4]
                                                                                                                                          Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C., Cabrera V.M., "Major genomic mitochondrial lineages delineate early human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=MTND1; Synonyms=ND1;
Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Human).
Homondarien.
Eukaryots, Metazea; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=81173052; Pubmed=7219534;
Anderson S., Bankier A.T., Barreell B.G., de Bruijn M.H.L.,
Coulson A.R., Drouin J., Eperon I.C., Nierlich D.P., Roe B.A.,
Sanger F., Schreier P.H., Smith A.J.H., Staden R., Young I.G.,
"Sequence and organization of the human mitochondrial genome.";
Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS ALA-87 AND ALA-168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUIM HUMAN STANDARD; PRT; 318 AA. P03886; Q37523; 21-UTL-1986 (Rel. 01, Created) Last sequence update) 05-UTL-2004 (Rel. 01, Last sequence update) 05-UTL-2004 (Rel. 44, Last annotation update) NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.5%; Score 131; DB 2; I 90.3%; Pred. No. 3.6e-09; Atrive 2; Mismatches 1;
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MEDLINE=95132634; PubMed=7530363;
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BMC Genet. 2:13-13(2001)
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Best Local Similarity
Matches 28; Conserv
                                                                                      SEQUENCE FROM N.A.
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   Mammalia; Euther
NCBI_TaxID=9606;
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NUIM_HUMAN
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WEDLINE=22406325; PubMed=12509511;
MEDLINE=22406325; PubMed=12509511;
MEDLINE=22406325; PubMed=12509511;
MEDLINE=22406325; PubMed=12509511;
MOSSEINI S., Brandon M., Essley K., Chen E., Brown M.D.,
A Sukernik R.I., Olckers A., Wallace D.C.;
The Matural selection shaped regional mcDNA variation in humans.";
The Argural Activity: NaDH + ubiquinone = NAD(+) + ubiquinol.
The Co. Matl. Acad. Sci. US. A. 100:177-176 (2003).
The Catalytic Activity: NADH + ubiquinone = NAD(+) + ubiquinol.
The Catalytic Activity: NADH + ubiquinone = NAD(+) + ubiquinol.
The Catalytic Activity: NADH + ubiquinone = NAD(+) + ubiquinol.
The Catalytic Activity: NADH + ubiquinone = NAD(+) + ubiquinone.
The Catalytic Activity of the complex I subunit I family.
The Catalytic Medles and The Catalytic I selectron transport; IEA.
The Catalytic NADHGh; 1.
The Procient Selones of Complexion NADH - 1:
The Catalytic NADHGh; 1.
The Procient Selones of Catalytic NADH - 1:
The Catalytic NADHGh; 1.
The Procient Selones of Catalytic NADHGh; 1.
The Reserve of Catalytic NA
   Huoponen K., Wallace D.C.;
"Mitochondrial DNA diversity in indigenous populations of southern extent Siberia, and the origins of native american haplogroups.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY615359; AAT17866.1; -.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 1.9e-09;
2, Mismatches 1, Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
NADH dehydrogenase subunit 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 1.
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Matches 28; Conservative
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Mitochondrion.
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Mitochondrion.
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RESULT 3
1085KT1
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Ingman M., Gyllensten U.; "Mitochondrial genome variation and evolutionary history of Australian
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PubMed=14766490; DOI=10.1007/S00414-004-0427-6;
Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J.;
Irwin J.A., Parsons T.J.;
"Single mucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 118:137-146(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-85188293; PubMed=3921850; Chomyn A., Mariottini P., Cleeter M.W.J., Ragan C.I., Matsuno-Yagi A., Hatefi Y., Doolittle R.P., Attardi G.; Ritanes of English reading trames of human mitochondrial DNA encode components of the respiratory-chain NADH dehydrogenase.";
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MEDLINE-91144615; PubMed=1900003;
Johns D.R., Berman J.;
"Alternative, simultaneous complex I mitochondrial DNA mutations in Leber's hereditary optic neuropathy.";
Biochem. Biophys. Res. Commun. 174:1324-1330(1991).
SEQUENCE FROM N.A.
MEDLINE=21012010; Pubmed=11130070; DOI=10.1038/35047064;
Ingman M., Kaessmann H., Paabo S., Gyllensten U.;
"Mitochondrial genome variation and the origin of modern humans.";
Nature 408:708-713(2000).
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WEDLINE-220266095, PubMed=19280999,
Howell N., Bindoff L., McCullough D.A., Kubacka I., Poulton J.,
Mackey D., Taylor L., Turnbull D.M.;
"Leber hereditary optic neuropathy: identification of the same
mitochondrial NDI meuropathy: pedigrees.";
Am. J. Hum. Genet. 49:939-950(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 130-318 FROM N.A. MEDILINES811077; PubMed=6260957; Sanger F., Coulson A.R., Barrell B.G., Smith A.J.H., Roe B.A., Cloning in single-stranded bacteriophage as an aid to rapid DNA
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MEDLINE-92070510; PubMed=1959619;
Majander A., Huoponen K., Savontaus M.-L., Nikoskelainen E.,
                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-22723755; PubMed=12840039; DOI=10.1101/gr.686603;
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Genome Res. 13:1600-1606(2003).
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RA Makagawa Y., Ikegami H., Yamato E., Takekawa K., Fujisawa T.,
RA Hamada Y., Uchigata Y., Miki T., Kumahara Y.;
RA Hamada Y., Uchigata Y., Miki T., Kumahara Y.;
RA Hamada Y., Uchigata Y., Miki T., Kumahara Y.;
RI dependent diabetes mellitus.;
RI dependent diabetes mellitus.;
RI Elocham. Biophys. Res. Commun. 209:664-668(1995).
C. -- CATALTYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
C. -- DISEASE: Defects in MTNDI are a cause of Leber's hereditary optic
atrophy. LHON [MIM:535000]; also known as Leber's optic
c. atrophy. LHON [MIM:535000]; also known as Leber's optic
atrophy. LHON is a maternally inherited disease resulting in acute
bilateral bindness due to retinal degeneration predominantly in
young men. Cardiac conduction defects and neurological defects
have also been described, resulting in optic nerve degeneration
and cardiac dysrhythmia.
C. -- DISEASE: Defects in MTNDI are a cause of mitochondrial
encephalomyopathy with lactic acidosis and stroke-like episodes
syndrome (MELAS) [MIM:54000]. MELAS is a genetically
heterogenious disorder, characterized by episodic vomiting,
selizures, and recurrent cerebral insults resembling strokes and
causing hemiparesis, hemianopsia, or cortical blindness.
C. -- DISEASE: Defects in MTNDI could be associated to mitochondrial
susceptibility to Alzheimer's disease (AD) [MIM:50200].
C. -- DISEASE: Defects in MTNDI could be associated with non-insulin-
dependent diabetes mellitus (NIDDM)
C. -- DISEASE: Defence in MTNDI complex I subunit I family.
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                                                                                                            human mitochondrial DNA and translation products:
                                                                                                                                                                                                                         MEDLINE-93038635; PubMed=1417830;
Johns D.R., Neufeld M.J., Park R.D.;
"An ND-6 mitochondrial DNA mutation associated with Leber hereditary
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94010883; PubMed=8104867; Shoffner J.M., Brown M.D., Tortoni A., Lott M.T., Cabell M.F., Mirra S.S., Beal M.F., Yang C.-C., Gearing M., Salvo R., Watte Juncos J.L., Hansen L.A., Crain B.J., Payad M., Reckord C.L.,
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Jaksch M., Hofmann S., Kaufhold P., Obermaier-Kusser B., Zierz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mitochondrial DNA variants observed in Alzheimer disease and
                                                             Marzuki S., Noer A.S., Lertrit P., Thyagarajan D., Kapsa R., Utthanaphol P., Byrne E., "Normal variants of human mitochondrial DNA and translation I the building of a reference data base.", Hum. Genet. 88:139-145(1991).
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[14]
VARIANTS PRO-205; CYS-255 AND PRO-288.
MEDLINE-92098084; PubMed=1757091;
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MEDLINE=95251666; PubMed=7733935;
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Genomics 17:171-184 (1993).
[17]
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                                                                                                                                                                                                                                                                                                        neuropathy.";
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Fri Nov 12 14:55:08 2004

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88.5%; Score 131; DB 2; Length 318;
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                                                                                                      Homo sapiens (Human).
Mitochondrion.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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PROSITE; PS00667; COMPLEXI.ND1 1; 1.
PROSITE; PS00668; COMPLEXI.ND1 2; 1.
Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
SEQUENCE 318 AA; 35669 MW; 2F7BD6C755CC295D CRC64;
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Pred. No. 3.6e-09;
2; Mismatches 1; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
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28; Conservative
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AAP89127.1;
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AAP89257.1;
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AAP89166.1;
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Mitochondrion.
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Best Local Similarity
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                                     AY339405;
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SEQUENCE FROM N.A.

Starikovskaya E.B., Sukernik R.I., Derbeneva O.A., Volodko N.V.,

A starikovskaya E.B., Sukernik R.I., Derbeneva O.A., Volodko N.V.,

A toroni A., Railace D.C.;

Huoponen K., Wallace D.C.;

"Mitochondrial DNA Diversity in Indigenous Populations of Southern

Fretent of Siberia, and the Origins of Native American Haplogroups.";

Ann. Hum. Genet. 0:0-0(2004).

C. -! CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C. -! SIMILARITY: Belongs to the complex I subunit 1 family.

EMBL, AYS19488 AAR31258.1, -

REBL, AYS19488 AAR31258.1, -

REBL, AYS19488; DAR31258.1, -

InterPro: IPRO0146; NADHGH; 1.

R PROSTIE: PS00466; COMPLEXI. ND1 1; 1.

PROSTIE: PS00466; COMPLEXI. ND1 1; 1.

PROSTIE: PS00667; COMPLEXI. ND1 1; 1.

PROSTIE: PS00667; COMPLEXI. ND1 1; 1.

PROSTIE: PS00667; CAMPLEXI. ND1 1; 1.

PROSTIE: PS00667; CAMPLEXI. ND1 2; 1.
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                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mitochondriton.
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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88.5%; Score 131; DB 2;
Best Local Similarity 90.3%; Pred. No. 3.6e-09;
Matches 28; Conservative 2; Mismatches 1;
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                                                                              NADH dehydrogenase subunit 1.
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PRELIMINARY;
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Best Local Similarity
Matches 28; Conserv
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Q6VH72
ID Q6VH72
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QERRM1
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Coble M.D., Just R.S., O'Callaghan J.B., Letmanyi I.H., Peterson C.T.,
Irwin J.A., Parsons T.J.;
Isingle nuclectide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.";
Inc. J. Legal Med. 0:0-0(2004).
Inc. J. Legal Med. 0:0-0(2004).
Inc. ATALYITC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
Inc. ATALYITC Relongs to the complex I subunit I family.
EMBL; AY495131; AAR93029.1;
GO:0005739; C:mitochondrian; IBA.
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-I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                      Gaps
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Mitochondation.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pfam; PF00146; NADHdh; 1.
PR005ITE; P800667; COMPLEXI_NDI_1; 1.
PR0SITE; P800668; COMPLEXI_NDI_2; 1.
Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
SEQUENCE 318 AA; 35690 MW; D483BIC561AB2F31 CRC64;
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88.5%; Score 131; DB 2; Length 31

Best Local Similarity 90.3%; Pred. No. 3.6e-09;

Matches 28; Conservative 2; Mismatches 1; Indels
                      Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
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05-UUL_2004 (TrEMBLrel. 27, Last sequence update)
05-UUL_2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
Best Local Similarity 90.3%; Pred. No. 3.6e-09;
Matches 28; Conservative 2; Mismatches 1;
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                                                                  1 ANLILLMVPILLAMAFLMLTERKILGYIOPR 31
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Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J.; O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
Int. J. Legal Med. 0:0-0(2004).
Int. J. AR495111 AAR975769.1;
--- SIMILARITY: Belongs to the complex I subunit I family.
EMBL, AX495123; AAR92925.1;
--- EMBL, AX495123; AAR930640.1;
--- EMBL, AX495123; AAR930640.1;
--- EMBL, AX495123; AAR930640.1;
--- EMBL, AX495123; AAR930640.1;
--- Carany AAR95123; AAR950640.1;
--- Carany AAR95123; AAR950640.1;
--- Carany AAR95123; AAR950640.1;
--- Carany AAR95123; AAR950640.1;
--- Carany AAR951240.1;
--- Carany
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Mitochondrion.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PERM; PF00146; NADHGh; 1.
PROSITE; PS00667; COMPLEX1 ND1 1; 1.
PROSITE; PS0068; COMPLEX1 ND2 1; 1.
RROSITE; PS0068; COMPLEX1 ND2 2; 1.
SMitochondrion; NAD; Oxidoctase; Transmembrane; Ubiquinone.
SEQUENCE 318 AA; 35660 NW; 2EC48962B4892D09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 318;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
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EMBL; AY495181; AAR93653.1;
EMBL; AY495183; AAR93705.1;
EMBL; AY495183; AAR93705.1;
EMBL; AY495184; AAR93718.1;
EMBL; AY495185; AAR93718.1;
EMBL; AY495105; AAR9374.1;
EMBL; AY495105; AAR9256.1;
GO; GO:0005739; C:mitochondrion; IEA.
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Fri Nov 12 14:55:08 2004

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YEQUENCE FROM N.A.

X PubMed=12949162.

A Mollanen J.S., Finnia S., Majamaa K.;

Tinneage-specific selection in human mtDNA: lack of polymorphisms in a segment of MTNDS gene in haplogroup J.";

Mol. Biol. Evol. 20:2133-2142(2003).

-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

-!- SIMILARITY: Belongs to the complex I subunit 1 family.

REBL; AX139545; AA990855.1; --

REBL; AX139545; AA990855.1; --

REBL; AX139546; AA990855.1; --

REPL; AX139546; AA990855.1; --

REPL; AX139546; AA99085.1; --

REPL; AX19746667; AA99085.1; --

REPL; AX19746667; AA99085.1; --

REPL; AX197466
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
VOBI_TaxID=9606;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Finnila S., Lehtonen M.S., Majamaa K.;
"Phylogenetic network for European mtDNA.";
Am. J. Hum. Genet. 68:1475-1484 (2001)
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Best Local Similarity 90.39
Matches .28; Conservative
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PubMed=14563219;
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Q6WQ94;
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A Train J.A., Parsons T.J.;

A Train J.A., Peterson C.T.;

I. Intrase the power of forensic testing in Caucasians.";

I. Int. J. Legal Med. 0:0-0(2004).

C. -- CAPALYIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C. -- SIMILARITY: Balongs to the complex I subunit I family.

REMEL, AV335589; AAP91460.1;

REMEL, AV495209; AAR93441.1;

REMEL, AV495209; AAR94441.1;

REMEL, AV33589; AAR94441.1;

REMEL, AV49500; AAR94441.1;

REMEL, AV33589; AAR94441.1;

REMEL, AV35889; AAR94441.1;

REMEL, AV38889; AAR9441.1;

REMEL, AV38889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moilanen J.S., Finnila S., Majamaa K.;
Moilanen J.S., Finnila S., Majamaa K.;
"Lineage-specific selection in human mtDNA: lack of polymorphisms in
segment of MTND5 gene in haplogroup J.";
Mol. Biol. Evol. 20:2132-2142(2003).
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                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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PROSITE; PS00667; COMPLEXI ND1 2; 1.
PROSITE; PS00668; COMPLEXI ND1 2; 1.
Mitochondrion; NAD; OCNEC ductase; Transmembrane; Ubiquinone.
SEQUENCE 318 AA; 35664 MW; 0895BFRGC65002FA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 318;
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                                        05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.5%; Score 131; DB 2; L 90.3%; Pred. No. 3.6e-09; iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21313109; PubMed=11349229;
Rinnila S., Lehtonen M.S., Majamaa K.;
"Phylogenetic network for European mtDNA.";
Am. J. Hum. Genet. 68:1475-1484 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; .318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=21313109; PubMed=11349229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Mitochondrion.
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Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12949126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=ND1
                                                                                                                                                                                   Name=ND]
          Q6VH72;
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Length 318;

; 0 "Mitochondrial DNA transit between West Asia and North Africa inferred Gaps Maca-Meyer N., Gonzalez A.M., Pestano J., Flores C., Larruga J.M., ; 0 Length 318; 1; Indels 88.5%; Score 131; DB 2; 90.3%; Pred. No. 3.6e-09; iive 2; Mismatches 1;

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MEDINE-2727375; PubMed=12840039;

MEDINE-2727375; PubMed=12840039;

MICOCONDITION OF AUGUSTANCE OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Kong Q.-P., Yao Y.-G., Sun C., Bandelt H.-J., Zhu C.-L., Zhang Y.-P.,
"Phylogeny of East Asian Mitochondrial DNA Lineages Inferred from
Complete Sequences.";
Am. J. Hum. Genet. 0:0-0(2003).
                                                                                                                                                                                                                                                                                                        Mitochondrion.
Wateropean Marazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Marmalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
WCBI_TaxID=9606;
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                                                                                      01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
02-071-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
                                       318 AA.
                                       PRT;
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                    Q7Y7U2
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Search completed: November 10, 2004, 13:38:23 Job time : 38.8532 secs

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117, Appl 117, Appl 117, Appl 117, Appl 117, Appl 117, Appl 118, A

Sequence Seq

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         US-08-095-068-15
US-08-095-068-17
US-08-140-721A-15
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US-09-499-039-133
US-09-549-001C-3486
US-08-671-757A-9
US-09-549-091C-3486
US-09-549-091C-3486
US-09-549-091C-3486
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US-09-549-091C-3486
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TYPE: amino acid
; TOPOLOGY: linear
US-09-097-889-17
STRANDEDNESS:
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US-09-097-889-17
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Sequence 4693, Ap
Sequence 21089, A
Sequence 25834, A
Sequence 5477, App
Sequence 5477, App
Sequence 42198, A
Sequence 42198, A
Sequence 20246, A
Sequence 14, Appl
Sequence 16, Appl
                                                                                                                November 10, 2004, 12:32:37; Search time 10.3627 Seconds (without alignments) 191.991 Million cell updates/sec
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              GenCore version 5.1.6
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1 LRLNITVWPTIITPILLTLFLITNRLITTR 30
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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RESULT 4
US-09-248-796A-21089

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J Sequence 21089

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Sequence 3814, Application US/09248796A

Sequence 3814, Application US/09248796A

SEQUENCE 51314, Application US/09248796A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

PRIOR PEDICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PRIOR OF SEQ ID NOS: 28208
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Pred. No. 10;
4; Mismatches 6; Indels
                                                                                                                                                   Length 440;
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14;
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Pred. No. 14;
7; Mismatches
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                                               TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 UMPTIITPILLTLFLITNR 25
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52 LWLLLLIPIFLTIFLIARR 70
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                                                                                                                                                     36.0%;
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Best Local Similarity 47.4%;
Matches 9; Conservative ,
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US-09-248-796A-21089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans
                                                                                                                                                     Query Match
Best Local Similarity 40.6
Matches 13; Conservative
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US-09-248-796A-25834
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SEQ ID NO 4693
LENGTH: 440
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ORGANISM:
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Sequence 4693, Application US/09583110
Sequence 46997, Application US/09583110
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHO0-079
CURRENT FILING DATE: 1200-05-26
RICK APPLICATION NUMBER: US 09/107,433
FRICK APPLICATION NUMBER: US 09/107,433
FRICK FILING DATE: 1998-06-30
FRICK APPLICATION NUMBER: US 60/085,131
FRICK FILING DATE: US 60/051,553
FRICK APPLICATION NUMBER: US 60/051,553
RECORD APPLICATION NUMBER: US 60/051,553
RECORD APPLICATION NUMBER: US 60/051,553
RECORD APPLICATION NUMBER: US 60/051,553
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                                                                                   Sequence 17, Application US/09098079
Sequence 17, Application US/09098079
Sequence 17, Application US/09098079
Setent No. 6489095
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Pahy, Boin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.3%; Score 102.5; DB 4; Length 68; 69.0%; Pred. No. 7.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READALLE FORM:
COMPUTER. FLOOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DESTRICT PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RENTITVMPTIITPILLTLFLITN-RLITT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QLNTTVWPTMITPMLLTLFLITQLFWLNT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.416
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO. 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 69.09
Matches 20; Conservative
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US-09-583-110-4693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: WA
                                                                             JS-09-098-079-17
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Sequence 26751, Application US/09248796A

Sequence 26751, Application US/09248796A

Sequence 26751, Application US/09248796A

SEQUENCE 2674137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WOCHEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,409
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26751

LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8270, Application US/09543681A

Patent No. 6605709

Patent No. 6605709

TITLE GRY BRETON

TITLE OF INVENTION:

PITLE OF INVENTION:

PITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT PILING DATE: 2000-04-05

PRIOR PILING DATE: 2000-04-05

PRIOR PILING DATE: 1999-04-09

SEQ ID NO 8270

LENGTH: 302
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                                                                                                                                                                                                                                                                                                                  Length 456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: | | : | | : | | 37 RRNPSMWMPLMIHQLRSHQVPLLIHPLWLTCYRVTNRRI 75
                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                Ouery Match
34.3%; Score 51.5; D
Best Local Similarity 30.6%; Pred. No. 31;
Matches 12; Conservative 6; Mismatches
                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SSCTWARE: Patentin Ver. 2.0
SEQ ID NO 42198
LENGTH: 456
                                                                                                                                                          TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LKTTLTPTLVVPILVT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Candida albicans
US-09-248-796A-26751
                                                                                                                                                                                                                                                                                                                                                                                                                    2 RLNTTVW-----
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                                                                                                                                       Sequence 5217, Application US/09198452A

Parent No. 6559294

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
FILE REPERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT PILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT; Homburger et al.

APPLICANT; Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REPERSENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 57472

LENGTH: 263
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.7%; Score 52; DB 4; Length 286; Best Local Similarity 50.0%; Pred. No. 16; Atches 13; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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30.8%; Pred. No. 18;
iive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-57472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) LOCATION: 1...286
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 LCLKQTKWSPIISPIKAFLYLFVVTN 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LRLNTTVWPTIITPI--LLTLFLITN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
209-270-767-57472
; Sequence 57472, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42198, Application US/09270767
Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Drosophila melanogaster
  TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.8
Matches 12; Conservative
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US-09-270-767-42198
                                                                                                       RESULT 6
US-09-198-452A-547
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à d Score 51;

34.0%;

Query Match

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(US-08-055-917-16
) Sequence 16, Application US/08055917
) Patent No. 5310875
) GENERAL INFORMATION:
    APPLICANT: Chang, Tse Wen; Chang, Nancy T.
    ITLE OF INVENTION: Peptides corresponding to membrane-bound IGA
) NUMBER OF SEQUENCES: 19
    CORRESPONDENCE: TANOX BIOSYSTEMS, INC.
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                                                                                                                                                                                           Score 49; DB 1;
Pred. No. 9.2;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 32.7%; Score 49; DB 38.27%; Pred. No. 9.2; Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMFUTER: IBM PS/2
OPENATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/055,917
FILING DATE: 11/4/1991
APPLICATION NUMBER: 07/788,120
FILING DATE: 11/4/1991
APPLICATION NUMBER: 07/786,120
FILING DATE: 11/4/1991
APPLICATION NUMBER: 07/455,080
FILING DATE: 12/22/1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: TINX89-04CCC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Tanox Biosystems, Inc. 10301 Stella Link Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-055-917-18
;. Sequence 18, Application US/08055917
                                                                                                                                                                                              Query Match 32.7%; Sc
Best Local Similarity 64.7%; Pr
Matches 11; Conservative 2;
            TELEFAX: (713) 664-8914
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VWPTIITPILLTLFLIT 23
                                                                                                                                                                                                                                                                                                                                  27 IMPTTİT--FLTLFLİS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 65 amino acids
TYPE: amino acid
TOPOLOGY: Linear
                                                                                                  ; TYPE: amino acid
; TOPOLOGY: Linear
US-08-055-917-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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APPLICANT: Kelth Weinerock et al

ITTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

IITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 107196.13

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

RIGH APPLICATION NUMBER: US 60/096,409

FRIGH FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 20246
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Patent No. 5310875
GENERAL INPORMATION:
APPLICANT: Chang, TEW Wen; Chang, Nancy T.
TITLE OF INVENTION: Peptides corresponding to membrane-bound IgA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tanox Biosystems, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                     11; Indels
Best Local Similarity 48.1%; Pred. No. 24;
Matches 13; Conservative 3; Mismatches
                                                                                                39 LREGFTVYRWALIPLLLLFLILGSLI 65
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                                                                1 LRENTTVWPTITTPILLTLFLITNRLI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Texas
COUNTRY: USA
ZIP: 77025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION NUMBER: US/08/055,917
                                                                                                                                                                                                                      Sequence 20246, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/788,120
FILING DATE: 11/4/1991
APPLICATION NUMBER: 07/455,080
FILING DATE: 12/22/1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LNTTVWPTIITPILLTLFLIT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Tanox Biosystems, STREET: 10301 Stella Link Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mirabel, Eric P. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston
                                                                                                                                                                                                       US-09-248-796A-20246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-248-796A-20246
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2; Gaps
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Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                      FILING DATE: 9/16/1991
APPLICATION NUMBER: 07/455,080
FILING DATE: 12/22/1989
ATTORNEY/AGENT INFORMATION:
NAME: Mirabel. Eric P.
REGISTRATION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: 71,213
REFERENCE/DOCKET NUMBER: TNX89-04DEE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 664-2288
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: November 10, 2004, 13:44:01
Job time : 10.3627 secs
7 VWPTIITPILLTEFLIT 23
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Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 LWPTTIT--FLTLFLIS
                      PRIOR APPLICATION DATA APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-095-068-14
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Patent No. 5362643

Patent No. 5362668

Patent No. 5362668

Patent No. 5362668

Patent No. 5362668

Patent No. 536268

                                        TITLE OF INVENTION: Peptides corresponding to membrane-bound IgA TITLE OF INVENTION: Peptides corresponding to membrane-bound IgA NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: 19
CORRESPONDENCE ADDRESS: 19
CORRESPONDENCE ADDRESS: 19
CONTY: HOUSEON STREIT: Texas
COUNTRY: USA
ZIP: 77025
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: Wordperfect 5.1
CURRENT APPLICATION NATE: WS/08/055,917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: TRX89-04CCC
TELECOMUNICATION INFORMATION:
TELEPHONE: (713) 664-2288
TELEPAX: (713) 664-8914
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.7%; Score 49; 55.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/788,120
APPLICATION NUMBER: 07/455,080
FILING DATE: 12/22/1989
ATTORNEY/AGENT INFORMATION:
NAME: Mitchel, Eric P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 TVWPTIITPILLTLFLIT 23
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Best Local Similarity 55.6
Matches 10; Conservative
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TOPOLOGY: Linear
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Sequence 337725, Sequence 547, App Sequence 5361, App Sequence 5392, App Sequence 3397, App Sequence 3997, App Sequence 3997, App Sequence 276546, Sequence 134, App Sequence 134, App Sequence 134, App Sequence 134, App Sequence 134, App Sequence 134, App Sequence 125321, Sequence 126321, Sequence 126321, Sequence 126321, Sequence 28156, Sequence 28156, Sequence 183989, Sequence 136989, Sequence 136989, Sequence 136989, Sequence 133, App Seq

Title: Perfect score: Sequence:

protein

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Run on:

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

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Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
7 US-10-425-115-337725
5 US-10-289-762-547
6 US-10-106-698-5592
4 US-09-946-143-2
6 US-09-946-13997
6 US-09-946-13997
6 US-09-946-13997
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6 US-09-948-199-276546
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8 US-10-424-599-276755
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9 US-10-424-599-280251
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100.0%; Score 150; DB 14;
Best Local Similarity 100.0%; Pred. No: 2.4e-13;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LRLNTTVWPTIITPILLTLFLITNRLITTR 30
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US-10-264-049-4146
Sequence 4146, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
     TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-27
   g
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Sequence 11, Appl
Sequence 13, Appl
Sequence 139, App
Sequence 189, App
Sequence 25622,
Sequence 245, App
Sequence 187835,
Sequence 11334,
Sequence 11334,
Sequence 15928,
Sequence 15621, App
Sequence 15621, App
                                                                                                                     November 10, 2004, 16:36:12; Search time 32.228 Seconds (without alignments) 328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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1: /cgn2_6/ptodata/1/pubpaa/DFT FUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/DFT Waw Publ.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/USO6_FUBGOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_FUBGOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_Waw Publ.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_Waw Publ.pep:*
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-264-049-4146

US-09-098-079-17

6 US-10-408-765A-139

6 US-10-408-765A-139

7 US-10-425-115-256252

5 US-10-424-599-187835

6 US-10-424-599-187835

6 US-10-424-599-187835

6 US-10-474-776-245

6 US-10-474-599-189528

6 US-10-369-493-15813

4 US-10-369-493-16212
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150
1 LRLNTTVWPTIITPILLTLFLITNRLITTR 30
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      1566620 segs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                   Length 68;
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Bradford W.
APPLICANT: Glasty M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERSENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
                                                                Indels
                Query Match 68.3%; Score 102.5; DB 9; Best Local Similarity 69.0%; Pred. No. 1.6e-06; Matches 20; Conservative 6; Mismatches 2;
                                                                                                           2 RENTIVAPTIITPILLILELIUN-RLITT 29
                                                                                                                                       3 QLNTTVWPTMITPMLLTLFLITQLKMLNT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURKENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 139
LENGTH: 68
TWEN
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; Sequence 1491, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                             RESULT 4
US-10-408-765A-139
US-10-408-139, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Sounitra S.
applICANT: Fahy, Boin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-408-765A-1491
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                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (55) ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids (98-10-264-049-4146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Herrnstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Greenger, William
APPLICANT: Greenger, William
APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIGGNOSTIC METHOD BASED ON QUANTIFICATION OF TITLE OF INVENTION: EXTRAMITOCHONDDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.0%; Score 103.5; DB 15; Length 65; Best Local Similarity 77.8%; Pred. No. 1.1e-06; Matches 21; Conservative 3; Mismatches 2; Indels 1;
HAPPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAINSH
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US (0/209,467)
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 NTTVWPTIITPILLTLFLITN-RLITT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-098-079-17
; Sequence 17, Application US/09098079
; Patent No. US20020064773A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_PEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear ... US-09-098-079-17
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US-10-474-776-245
US-10-474-776-245
US-10-474-776-245
Sequence 245, Application US/10474776
Publication No. US20040110181A1
GENERAL INFORMATION:
GENERAL INFORMATION:
HAPPLICANT: Wyeth
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
CURRENT APPLICATION UNMERS: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
SEQ ID NO 245
LENGTH: 441
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US-10-424-599-159528

US-10-424-599-159528

SUBJUCTION NO. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 105/2021 8021(53223) 803-04-28

UNMERN APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ENDITED THE OF INVENTION: BOY NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
FEATURE:
COMMENTION: Clone ID: PAT_MRT3847_115073C.1.pep
US-10-424-599-159528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.0%; Score 54; DB 16; Best Local Similarity 40.6%; Pred. No. 43; Matches 13; Conservative 7; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.3%; Score 53; DB 15; Best Local Similarity 50.0%; Pred. No. 10; Matches 9; Conservative 5; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 INTALLFTFPTVLNPIMLIPFIATPTINALIT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LNTTV---WPTIITPILLTLFLIT---NRLIT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 111334, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae US-10-474-776-245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LRLNTTVWPTIITPILLT 18
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Barbazuk, Brad
Li, Ping
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-10-437-963-111334
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| Publication No. US20040031072A1
| GENERAL INNORMATION:
| GENERAL INNORMATION:
| GENERAL INNORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Alou Yihua
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: 38-21 (53223) B
| CURRENT APPLICATION NUMBER: US/10/424,599
| CURRENT APPLICATION NUMBER: US/10/424,599
| VURRENT FILING DATE: 2003-04-28
| SEQ ID NO 187835
                                                                                                                       RESULT 6
103-10-425-115-256252
1 Sequence 256252, Application US/10425115
1 Publication No. U320040214272A1
1 GENERAL INFORMATION:
1 APPLICANT: La Rosa, Thomas J.
2 APPLICANT: Cao, Yinna
2 APPLICANT: Cao, Yinna
3 APPLICANT: Cao, Yinna
4 APPLICANT: Cao, Yinna
3 APPLICANT: Cao, Yinna
4 APPLICANT: Cao, Yinna
5 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
5 TITLE OF INVENTION: Plants
6 TITLE PERFERENCE: 38-21(53.22) B
7 CURRENT APPLICATION NUMBER: U5/10/425,115
7 CURRENT FILING DATE: 2003-04-28
7 NUMBER OF SEQ ID NOS: 369326
7 SEG ID NO 256252
7 LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_140628C.1.pep
US-10-424-599-187835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
40.3%; Score 60.5; DB 17;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 14; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: MR74577_165293C.1.pep
US-10-425-115-256252
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50.0%; Pred. No. 5.1;
tive 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(86)
OTHER INFORMATION: unsure at all Xaa locations
          10 NTXVWPXIXFPITXLXLFLIT 30
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Best Local Similarity 50.0
Matches 10; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
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US-10-424-599-187835
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34.7%; Score 52; DB 17; Length 43;
                                                                                                                                         TYPE: PRT ORGANISM: Xanthomonas campestris
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                                                                                                                                                                                                                                                                           35.3%;
Best Local Similarity 40.0%;
Matches 10; Conservative 6
                       NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15831
LENGTH: 430
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ORGANISM: Zea mays
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; Sequence 15462, Application US/10369493
; Publication No. US20030233675A1
; Pablication No. US20030233675A1
; Pablication No. US20030233675A1
; APPLICANT: Cao, Yongwei
; APPLICANT: Galdman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
TITLE OF INVENTION: EAPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: DANTS WITH IMPROVED PROPERTIES
; TILE REFERENCE: 38-10(52052)
; FILE REFERENCE: 38-10(52052)
; CURRENT FALING DATE: 2003-02-28
; CURRENT FILING DATE: 2003-02-28
; RAIOR APPLICATION NUMBER: US 60/360,039
; RAIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 111334 LENGTH: 379
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Publication No. US2003023675A1

GENERAL INFORMATION:

APPLICANT: Goldmen, Barry S.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_15321C.1.pep
US-10-437-963-111334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 40.0
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Xiandeng
TILLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 10/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subjection No. US20040214272A1

Subjection No. US20040214272A1

Subjection No. US20040214272A1

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongheic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants
ITILE OF INVENTION: Plants
TITLE OF INVENTION: 105.228
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 369326

IENGTH: 43

LENGTH: 43
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                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.3%; Score 53; DB Best Local Similarity 40.0%; Pred. No. 57; Matches 10; Conservative 6; Mismatches
                                                 6; Mismatches
Score 53;
Pred. No. 5
                                                                                                                                       103 LLATVWPALPVPMLASVFMATFTVI 127
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; Sequence 16212, Application US/10369493
; Publication No. US20030233675A1
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RESULT 15
US-10-289-762-547
US-10-289-762-547
Sequence 547, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: GTAIFfais, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NOS: 6849
SEQ ID NOS: 47
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                         2; Gaps
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                           8; Indels
Best Local Similarity 50.0%; Pred. No. 7.4; Matches 14; Conservative 4; Mismatches
                                                              4 NITUWPTIITPILLTLFLI--TNRLITT 29
                                                                                            11 NITHEPSILIPKPPTLFFIIPSNSTITT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
1 LOCATION: 1...286
1 OTHER INVERMATION: Xaa=unknown or other US-10-289-762-547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Chlamydia pneumoniae
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November 10, 2004, 12:29:32; Search time 6.68394 Seconds (without alignments) 431.857 Million cell updates/sec
GenCore version 5.1.6
(c).1993 - 2004 Compugen Ltd.
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                    Copyright
                                                                                OM protein
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US-10-092-750-27 150 1 LRLNTTVWPTIITPILLTLFLITNRLITTR 30 Title: Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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hypothetical prote	. H+-transporting tw	ABC transporter, m	trehalose/maltose	conserved hypothet	hypothetical prote	H+-transporting tw	H+-transporting tw	H+-transporting tw	probable lprF prot	probable transport	membrane protein y	probable transport	Sodium, galactoside	flagellar biosynth	flagellar biogenes
H72557	PWHU6	AC2749	B97530	D89974	B70543	E58850	S41839	T11484	E70957	D85826	D64966	086065	AC0122	C81361	A49217
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ALIGNMENTS

RESULT 1 PWHU8		
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - human mi	- human	Ξ
N;Alternate names: hydrogen ion-transporting ATP synthase protein 8	protein	œ

itochondrion

N;Alcernate names: hydrogen ion-transporting ATP syntnase process of Species allocations of Species anitochondrion Homo sapiens (man)
(S;Species 22-May-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
(C;Accession: A01062; 180237
(C;Accession: A) Bankier, A.T.; Barrell, B.G.; de Bruijn, M.H.L.; Coulson, A.R.; Drouin, C

Nature 290, 457-465, 1981

A; Title: Sequence and organization of the human mitochondrial genome.

A; Reference number: A00151; MUID:81173052; PMID:7219534

A; Reference number: A00162

A; Molecule type: DNA

A; Residues: 1-68 - AND>
A; Cross-references: UNPROT: P03928; GB:J01415; GB:M12548; GB:M58503; GB:M63932; R; Horai, S: Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.

Proc. Natl. Acad. Sci. U.S.A. 92, 532-536, 1995

A; Title: Recent African origin of modern humans revealed by complete sequences of hominon A; Accession: 180333.

A;Status: translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-31,'S',33-68 <RES>
A;Cross-references: GB:D38112; NID:g644480; PIDN:BAA07294.1; PID:g704445
G;Generics:
A;Gene: GDB:MTATP8

A)Cross-references: GDB:118898; OMIM:516070
A;Map position: MTH8366-8572
A;Genome: mitochondrion
A;Genotic code: SGCI
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; ~hydrolase; membrane-associated complex; mitochondrion; oxic 68;

Gapa Match 68.3%; Score 102.5; DB 1; Length Local Similarity 69.0%; Pred. No. 3.9e-07; es 20; Conservative 6; Mismatches 2; Indels

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2 RINTTVWPTIITPILLTLFLITN-RLITT 29 g ઠે

RESULT 2 E59153

H-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - western lowland gorilla mitor N,Alternate names: hydrogen ion-transporting ATP synthase protein 8 C;Species: mitochondrion Gorilla gorilla gorilla (western lowland gorilla) C;Date: 03.Dec-1999 #sequence_revision 03.Dec-1999 #text_change 03.Jun-2002 C;Accession: E59153 R;Xu, X.; Arnason, U. Mol. Biol. Evol. 13, 691-698, 1996

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H-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - pygmy chimpanzee mitochondric C;Species: mitochondrion Pan paniscus (pygmy chimpanzee, bonobo) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T14147 Protai, S: Hayeaska, K:; Kondo, R:; Tsugane, K:; Takahata, N. Proc. Natl. Acad. Sci. U.S.A. 92, 532-536, 1995 A;Title: Recent African origin of modern humans revealed by complete sequences of hominoi A;Reference number: 159384; MulD:95132634; PMID:7530363 A;Accession: T14147 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Nebcule type: DNA A;Residues: 1-68 <-NOR>
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C; Date: 31.May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C; Accession: 137051
R; Horai, S.; Satta, Y.; Hayasaka, K.; Kondo, R.; Inoue, T.; Ishida, T.; Hayashi, S.; Take A; Moll. Space in Hominoidea revealed by mitochondrial DNA genealogy.
A; Title: Man's place in Hominoidea revealed by mitochondrial DNA genealogy.
A; Reference number: 137047; MUID:92389366; PMID:1518083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Genome: mitochondrion
A;Genotic code: SGC1
C;Superfamily: H+-tsransporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
C.Superfamily: H+-transporting ATP synthase protein 8
C.Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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A,Genteic code: SGCI
C,Superfamily: H+-transporting ATP synthase protein 8
C,Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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                                                                                                                                        Length 68;
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                                                                                                                                        Score 96; DB 2;
Pred. No. 3e-06;
                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                       2 RENTTVWPTITTPILLTLFLIT 23
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                                                                                                                                        Query Match
Best Local Similarity 77.3%;
Matches 17; Conservative
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T14147
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H-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - gorilla mitochondrion C; Species: mitochondrion Gorilla gorilla (gorilla)
C; Species: mitochondrion Gorilla gorilla (gorilla)
C; Date: 20-8ep-1999 #sequence_revision 20-8ep-1999 #text_change 09-Jul-2004
C; Accession: T14024
R; Horai, S:; Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R; Horai, S:, Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R; Horai, S:, Hayasaka, K.; Mondo, R.; Tsugane, K.; Takahata, N.
R; Horai, S:, Hayasaka, K.; Mondo, R.; Tsugane, K.; Takahata, N.
A; Attic: Recent African origin of modern humans revealed by complete sequences of homing A; Recenteen number: IS984; MulD:95132634; MulD:95132634; MulD:95132634; A; Accession: T14034
A; Accession: T14034
A; Accession: T14034
A; Accession: T14034
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H-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - chimpanzee mitochondrion C;Species: mitochondrion Pan troglodytes (chimpanzee)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14197
R;Horai, S: Hayasaa, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R;Horai, S: Hayasaa, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R;Horai, S: Hayasaa, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R;Horai, S: Hayasaa, M. Sando, R.; Sando, R.; Tsugane, K.; Takahata, N.
R;Horai, S.; Hayasaa, M. Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; Sando, R.; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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    A,Title: A complete sequence of the mitochondrial genome of the Western lowland gorilla. A,Reference number: Z17269; MUID:96212991; PMID:8676744
A;Accession: E59153
A;Status: preliminary; nucleic acid sequence not shown; translation not shown; translate A;Molecule type: DNA
A;Residues: 1-68 <XUX>
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A Genetic code: SGC:
C. Superfamily: H+-transporting ATP synthase protein 8
C. Superfamily: H+-transporting ATP synthase; membrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                    A;Cross-references: GB.X93347; NID:g1304307; GSPDB:GN00106
A;Cross-references: GB.Mank, November 1995
A;Note: this translation is not annotated in GenBank entry GGMITG, release 114.0
C;Genetics:
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A;Cross-references: UNIPROT:Q34571; EMBL:D38114; PIDN:BAA07304.1

A; Molecule type: DNA A; Residues: 1-68 <HOR>

Query Match 64.7%; Score 97; DB 2; Length 68; Best Local Similarity 81.8%; Pred. No. 2.2e-06; Matches 18; Conservative 3; Mismatches 1; Indels

A; Gene: ATPase8

3 OLNITVWPIMIAPMLLTLFLIT 24

g

Query Match 64.7%; Score 97; DB 2; Length 68; Best Local Similarity 81.8%; Pred. No. 2.2e-06; Matches 18; Conservative 3; Mismatches 1; Indels

ò g RESULT

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-68 <HOR> A;Cross-references: UNIPROT:Q35647; EMBL:D38113; PIDN:BAA07300.1 C;Genetics:

A;Genome: mitochondrion A;Genetic code: SGC1

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Cjacession: Al1421
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A,Residues: 1-66 <AND>
A,Cross-Actors: 1-66 <AND>
A,Cross-Lini, Malker, U.E.
EMBO J. 5, 2003-2008, 1986
                                               Cross-references: UNIPROT: Q9ZXYO; EMBL: Y18001; NID: g4049475; PIDN: CAA76998.1; PID: g4045;
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                                                                                                                                                           A;Genome: mitochondrion
A;Genetic code: SGCI
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
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C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A01063; A25474; D3956
J. Mol. Biol. 156, 683-717, 1982.
J. Mol. Biol. 156, 683-717, 1982.
A;Reference number: A00152; MUID:83010260; PMID:7120390
A;Reference number: A00152; MUID:83010260; PMID:7120390
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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Pred. No. 0.56;
5; Mismatches 5; Indels
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Biochemistry 30, 5369-5378, 1991
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91 INRNITATIIVGIILTLFLIAGTII 115
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A,Molacule type: protein
A,Residues: 1-37;45-50;52-53 <FEA>
R,Walker, J.E.; Lutter, R.; Dupuis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.3%;
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Best Local Similarity 54.5%;
Matches 12; Conservative 9
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Best Local Similarity 48.0
Matches 12, Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-169 <GLA>
Residues: 1-68 <ARN>
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PWBO8
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H+-transporting two-sector ATPase (BC 3.6.3.14) protein 8 - baboon mitochondrion

C,Species mitochondrion Papio hamadryas (baboon)

C,Species mitochondrion Papio hamadryas (baboon)

C,Accession: Tillio

C,Accession: Tillio

R;Armason, U.; Gullberg, A.; Janke, A.

J. Mol. Bvol. 47, 718-727, 1998

A;Ttle: Molecular timing of primate divergences as estimated by two non-primate calibra A;Reference number: Z17277; MUD:99065765; PMID:9847414

A;Accession: Tillio

A;Accession: Tillio

A;Accession: Tillio

A;Molecule type: DNA
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H.-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - common gibbon mitochondrion C; Species: mitochondrion Hylobates lar (common gibbon, white-handed gibbon)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11837
C;Accession: T11837
A;Accession: T1837
A
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A,Genetic oce: SGCI
C,Superfamily: H+-transporting ATP synthase protein 8
C,Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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A;Genetic code: SGC1
C;Superfamiloy: H+-Tensporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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                                   H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - orangutan mitochondrion Cispecies: mitochondrion Pongo pygmaeus (orangutan)
Cibacession: Tal443
Riborai, S.; Hayssaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
Riborai, S.; Hayssaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
Proc. Natl. Acad. Sci. U.S.A. 92, 532-536, 1995
A:Title: Recent African origin of modern humans revealed by complete sequences of hom A:Title: Recent African origin of modern humans revealed by complete sequences of hom A:Tatus: preliminary; translated from GB/EMBL/DDBJ
A:Accession: T14143
A:Accession: T14143
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Pred. No. 0.00017;
2; Mismatches 4; Indels
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Best Local Similarity 72.7%;
Matches 16; Conservative
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les 15; Conservative
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A; Molecule type: protein A; Residues: 1-5 <WAL> C; Genetics:

A; Genome: mitochondrion

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Pypotherical protein norB-1 [imported] - Sulfolobus solfataricus ()Species: Sulfolobus solfataricus ()Species: Sulfolobus solfataricus ()Species: Sulfolobus solfataricus ()Species: Sulfolobus solfataricus ()Species: Amay-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: A99316 ()Apocession: Apocession: Apoc
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Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Ricoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, S709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Reference number: A97872; MUID:21429245; FMID:11544234
A;Accession: E97924
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A)Cross-references: UNIFROT:097XY4; GB:AB006641; NID:913814802; PIDN:AAK41784.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Cross-references: UNIPROT: Q8DQ23, GB: AE007317; PIDN: AAK99225.1; PID: 915457986; GSPDB: GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: PTS-EII
C;Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-depende
                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)
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                                        Length 440;
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                                        DB 2;
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7, Mismatches
                                                                                                          7; Mismatches
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Pred. No.
                                        Score 54;
Pred. No.
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278 WPSIVIPVVLILLVVNN 294
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                                36.0%;
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                                                                                                                  13; Conservative
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Best Local Similarity 40.6'
Matches 13; Conservative
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Best Local Similarity
7; Conserve
                                        Query Match
Best Local Similarity
Matches 13; Conserv
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A:Molecule type: DNA
A:Residues: 1-441 <KUR>
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H95054
PTS system, cellobiose-specific IIC component [imported] - Streptococcus pneumoniae (str. C; Species: Streptococcus pneumoniae
C; Species: Streptococcus pneumoniae
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C; Accession: H95054
R; Tettelin, H: Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, anson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Reference number: A95000; MUID:21357209; PMID:11463916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-395 -KUR>
A;Cross-references: UNIPROT:Q97HE0; GB:AE001437; PIDN:AAK80031.1; PID:g15025060; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                         A;Genetic code: SGC1
C;Supertfamily: H+-transporting ATP synthase protein 8
C;Seywords: ATP biosynthesis; blocked amino end; hydrolase; membrane-associated complex;
F;I/Wodified site: blocked amino end (Wet) (probably formylated) #status experimental
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C;Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-depend
A;Title: Identification of the subunits of F-IF-0-ATPase from bovine heart mitochondria.
A;Reference number: A39566; MUID:91242449; PMID:1827992
A;Accession: D39566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stage IV sporulation protein B, SpoIVB [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C; Accession: D97155 R; Nolling, J.; Breton, G; Omelchenko, M.V.; Markarcva, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
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A,Cross-references: UNIPROT:097SB2; GB:AE005672; PIDN:AAK74633.1; PID:g14971945; GSPDB:
A,Experimental source: strain TIGR4
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C;Superfamily: Bacillus subtilis stage IV sporulation protein spoIVB
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Pred. No. 1.4;
6; Mismatches 5; Indels
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llarity 47.4%; Pred. No. 8;
Conservative 7; Mismatches
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Query Match Best Local Similarity

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November 10, 2004, 12:27:34 ; Search time 36.6321 Seconds (without alignments) 471.205 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                             OM protein - protein search, using sw model
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US-10-092-750-27 150 1 LRLNTTVWPTIITFILLTLFLITURLITTR 30 1825181 seqs, 575374646 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES	QI	TP8 HUMAN	QGRKZG	Q6RLZ4	QERMII	QGRNJ6	Q7YCD6	Q7YEE7	Q7YEG9	Q85KT5	Q85KZ3	95NH85	Q94P44	AAL54388	441	142	144	44	AAL54479	454	157	AAL54583	159	460	462	ぜ	479	0	AAN14540	155	9	AAN14573
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ALIGNMENTS

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AY339482;
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AY339485;
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified another statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Irwin J.A., Parsons T.J.,
"Single nucleotide polymorphisms over the entire mtDNA genome that
"Single nucleotide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.",
[1]
VARIANTS PRO.118:137-146(2004).
[7]
WARIANTS PRO.17 AND SER-21.
WEDLINE=92098084; PubMed=1757091;
MATZUKI S., Noer A.S., Lerrit P., Thyagarajan D., Kapsa R.,
Utthanaphol P., Byrne E.,
"Normal variants of human mitochondrial DNA and translation products:
the building of a reference data base.";
Hum. Genet. 88:139-145(1991).
                                                                                                                                                                                                                                                          genome.";
Nucleic Acids Res. 26:967-973(1998).
-!- FUNCTION: This is one of the chains of the nonenzymatic component
- (CP(0) subunit) of the mitcohondrial ATPase complex.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                          [8]
VARIANT THR-28.
WREDLINE=99127994; PubMed=9461455;
Rieder M.J., Taylor S.L., Tobe V.O., Nickerson D.A.;
Rieder M.J., Taylor S.L., Tobe V.O., Nickerson D.A.;
"Automating the identification of DNA variations using quality-based fluorescence re-sequencing: analysis of the human mitochondrial
                                                                                                                                                                                                                                                                                                                          EMBL; JO1415; AAB58947.1;
EMBL; VO0662; CAAZ4030.1;
EMBL; AV339402; AAP89040.1;
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AAP89248.1;
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AAP89352.1;
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AAP89326.1;
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AAP89430.1;
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AY339418;
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AAP9900.2.1;
AAP900.2.1;
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